GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 04:38:45 ; Search time 33 Seconds
(without alignments)
511.128 Million cell updates/sec

Title: US-09-918-029-19
Perfect score: 55
Sequence: 1 gtacattgacctagtgccgc.....gcggcactaggtcaatcgat 55

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	55	100.0	55	2	US-08-793-170-19	Sequence 19, Appl
	2	55	100.0	55	3	US-08-892-873-19	Sequence 19, Appl
	3	55	100.0	55	4	US-09-334-765A-19	Sequence 19, Appl
	4	55	100.0	55	4	US-09-356-575E-19	Sequence 19, Appl
	5	55	100.0	55	4	US-09-333-820-19	Sequence 19, Appl
	6	55	100.0	55	4	US-09-358-036-41	Sequence 41, Appl
	7	55	100.0	55	4	US-09-097-239-41	Sequence 41, Appl
c	8	51	92.7	55	2	US-08-793-170-20	Sequence 20, Appl
c	9	51	92.7	55	3	US-08-892-873-20	Sequence 20, Appl
c	10	51	92.7	55	4	US-09-334-765A-20	Sequence 20, Appl
c	11	51	92.7	55	4	US-09-356-575E-20	Sequence 20, Appl
c	12	51	92.7	55	4	US-09-333-820-20	Sequence 20, Appl
c	13	51	92.7	55	4	US-09-358-036-42	Sequence 42, Appl
c	14	51	92.7	55	4	US-09-097-239-42	Sequence 42, Appl
	15	47.4	86.2	50	2	US-08-793-170-17	Sequence 17, Appl
	16	47.4	86.2	50	3	US-08-892-873-17	Sequence 17, Appl
	17	47.4	86.2	50	4	US-09-334-765A-17	Sequence 17, Appl
	18	47.4	86.2	50	4	US-09-356-575E-17	Sequence 17, Appl
	19	47.4	86.2	50	4	US-09-333-820-17	Sequence 17, Appl
	20	47.4	86.2	50	4	US-09-358-036-39	Sequence 39, Appl
	21	47.4	86.2	50	4	US-09-097-239-39	Sequence 39, Appl
	22	43.4	78.9	45	2	US-08-793-170-22	Sequence 22, Appl
	23	43.4	78.9	45	3	US-08-892-873-22	Sequence 22, Appl
	24	43.4	78.9	45	4	US-09-334-765A-22	Sequence 22, Appl
	25	43.4	78.9	45	4	US-09-333-820-22	Sequence 22, Appl
	26	43.4	78.9	45	4	US-09-358-036-47	Sequence 47, Appl
	27	43.4	78.9	45	4	US-09-097-239-47	Sequence 47, Appl
c	28	43.4	78.9	50	2	US-08-793-170-18	Sequence 18, Appl
c	29	43.4	78.9	50	3	US-08-892-873-18	Sequence 18, Appl
c	30	43.4	78.9	50	4	US-09-334-765A-18	Sequence 18, Appl
c	31	43.4	78.9	50	4	US-09-356-575E-18	Sequence 18, Appl
c	32	43.4	78.9	50	4	US-09-333-820-18	Sequence 18, Appl
c	33	43.4	78.9	50	4	US-09-358-036-40	Sequence 40, Appl
c	34	43.4	78.9	50	4	US-09-097-239-40	Sequence 40, Appl
c	35	42.2	76.7	55	2	US-08-793-170-19	Sequence 19, Appl
	36	42.2	76.7	55	2	US-08-793-170-20	Sequence 20, Appl
c	37	42.2	76.7	55	3	US-08-892-873-19	Sequence 19, Appl
	38	42.2	76.7	55	3	US-08-892-873-20	Sequence 20, Appl
c	39	42.2	76.7	55	4	US-09-334-765A-19	Sequence 19, Appl
	40	42.2	76.7	55	4	US-09-334-765A-20	Sequence 20, Appl
c	41	42.2	76.7	55	4	US-09-356-575E-19	Sequence 19, Appl
	42	42.2	76.7	55	4	US-09-356-575E-20	Sequence 20, Appl
c	43	42.2	76.7	55	4	US-09-333-820-19	Sequence 19, Appl
	44	42.2	76.7	55	4	US-09-333-820-20	Sequence 20, Appl
c	45	42.2	76.7	55	4	US-09-358-036-41	Sequence 41, Appl

ALIGNMENTS

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RESULT 1
US-08-793-170-19
; Sequence 19, Application US/08793170
; Patent No. 5994128
;  GENERAL INFORMATION:
;    APPLICANT:  FALLAUX et al.
;    TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT
;    TITLE OF INVENTION:  ADENOVIRUS TO BE USED IN GENE THERAPY
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
;      STREET:  260 SHERIDAN AVENUE, PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,170
;      FILING DATE:  25-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO 97/00326
;      FILING DATE:  14-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201728.3
;      FILING DATE:  26-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201611.1
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.002.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-3377
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  55 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-793-170-19
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  Query Match             100.0%;  Score 55;  DB 2;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55


RESULT 2
US-08-892-873-19
; Sequence 19, Application US/08892873
; Patent No. 6033908
;  GENERAL INFORMATION:
;    APPLICANT:  FALLAUX et al.
;    TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT
;    TITLE OF INVENTION:  ADENOVIRUS TO BE USED IN GENE THERAPY
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
;      STREET:  260 SHERIDAN AVENUE, PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/892,873
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/793,170
;      FILING DATE:  25-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO 97/00326
;      FILING DATE:  14-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201728.3
;      FILING DATE:  26-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201611.1
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.002.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-3377
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  55 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-892-873-19

  Query Match             100.0%;  Score 55;  DB 3;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55


RESULT 3
US-09-334-765A-19
; Sequence 19, Application US/09334765A
; Patent No. 6238893
; GENERAL INFORMATION:
;  APPLICANT:  Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO BE USED
;  TITLE OF INVENTION:  IN GENE THERAPY
;  FILE REFERENCE:  3833.2US
;  CURRENT APPLICATION NUMBER: US/09/334,765A
;  CURRENT FILING DATE:  1999-06-16
;  PRIOR APPLICATION NUMBER:  US 08/793,170
;  PRIOR FILING DATE:  1997-03-25
;  PRIOR APPLICATION NUMBER:  PCT/NL96/00244
;  PRIOR FILING DATE:  1996-06-14
;  PRIOR APPLICATION NUMBER:  EP 95201728.3
;  PRIOR FILING DATE:  1995-06-26
;  PRIOR APPLICATION NUMBER:  EP 95201611.1
;  PRIOR FILING DATE:  1995-06-15
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  Corel WordPerfect 8.0
; SEQ ID NO 19
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: PCT primer HP/cla1
US-09-334-765A-19

  Query Match             100.0%;  Score 55;  DB 4;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55


RESULT 4
US-09-356-575E-19
; Sequence 19, Application US/09356575E
; Patent No. 6265212
; GENERAL INFORMATION:
;  APPLICANT:  Fallaux, Frits
;  APPLICANT:  Hoeben, Robert
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  van der Eb, Alex
;  APPLICANT:  Schouten, Govert
;  TITLE OF INVENTION:  PACKAGING SYSTEMS
;  FILE REFERENCE:  2578-3935US
;  CURRENT APPLICATION NUMBER: US/09/356,575E
;  CURRENT FILING DATE:  1999-07-19
;  PRIOR APPLICATION NUMBER:  US 08/793,170
;  PRIOR FILING DATE:  1997-03-25
;  PRIOR APPLICATION NUMBER:  PCT/NL96/00244
;  PRIOR FILING DATE:  1996-06-14
;  PRIOR APPLICATION NUMBER:  EP 95201611.1
;  PRIOR FILING DATE:  1995-06-15
;  PRIOR APPLICATION NUMBER:  EP 95201728.3
;  PRIOR FILING DATE:  1995-06-26
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Unknown
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;   FEATURE:
;   OTHER INFORMATION: Derived from Adenovirus
US-09-356-575E-19

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  Best Local Similarity   100.0%;  Pred. No. 7.8e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55


RESULT 5
US-09-333-820-19
; Sequence 19, Application US/09333820A
; Patent No. 6306652
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT: Hoeben, Robert C.
;  APPLICANT: Bout, Abraham
;  APPLICANT: Valerio, Domenico
;  APPLICANT: Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO BE USED IN
;  TITLE OF INVENTION: GENE THERAPY
;  FILE REFERENCE: 3833.1US
;  CURRENT APPLICATION NUMBER: US/09/333,820A
;  CURRENT FILING DATE: 1999-06-15
;  EARLIER APPLICATION NUMBER: US 08/793,170
;  EARLIER FILING DATE: 1997-03-25
;  EARLIER APPLICATION NUMBER: PCT/NL96/00244
;  EARLIER FILING DATE: 1996-06-14
;  EARLIER APPLICATION NUMBER: EP 95201728.3
;  EARLIER FILING DATE: 1995-06-26
;  EARLIER APPLICATION NUMBER: EP 95201611.1
;  EARLIER FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 19
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: PCT primer HP/clal
US-09-333-820-19

  Query Match             100.0%;  Score 55;  DB 4;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55


RESULT 6
US-09-358-036-41
; Sequence 41, Application US/09358036
; Patent No. 6340595
; GENERAL INFORMATION:
;  APPLICANT: Vogels, Ronald
;  APPLICANT: Bout, Abraham
;  APPLICANT: van Es, Helmuth
;  APPLICANT: Schouten, Govert
;  TITLE OF INVENTION: High Throughput Screening of Gene Function Using
;  TITLE OF INVENTION: Adenoviral Libraries for Functional Genomics
;  TITLE OF INVENTION: Applications
;  FILE REFERENCE: 21834108
;  CURRENT APPLICATION NUMBER: US/09/358,036
;  CURRENT FILING DATE: 1999-07-21
;  EARLIER APPLICATION NUMBER: US 09/097,239
;  EARLIER FILING DATE: 1995-07-25
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-358-036-41

  Query Match             100.0%;  Score 55;  DB 4;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 7
US-09-097-239-41
; Sequence 41, Application US/09097239
; Patent No. 6413776
;  GENERAL INFORMATION:
;    APPLICANT:  VOGELS, RONALD,
;    APPLICANT:  BOUT, ABRAHAM,
;    APPLICANT:  VAN ES, HELMUTH HG,
;    APPLICANT:  SCHOUTEN, GOVERT
;    TITLE OF INVENTION:  HIGH THROUGHPUT SCREENING OF GENE
;    TITLE OF INVENTION:  FUNCTION USING ADENOVIRAL LIBRARIES FOR FUNCTIONAL
;    TITLE OF INVENTION:  GENOMICS APPLICATIONS
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/097,239
;      FILING DATE:  12-JUN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.008.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  55 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-09-097-239-41

  Query Match             100.0%;  Score 55;  DB 4;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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RESULT 8
US-08-793-170-20/c
; Sequence 20, Application US/08793170
; Patent No. 5994128
;  GENERAL INFORMATION:
;    APPLICANT:  FALLAUX et al.
;    TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT
;    TITLE OF INVENTION:  ADENOVIRUS TO BE USED IN GENE THERAPY
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
;      STREET:  260 SHERIDAN AVENUE, PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,170
;      FILING DATE:  25-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO 97/00326
;      FILING DATE:  14-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201728.3
;      FILING DATE:  26-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201611.1
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.002.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-3377
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  55 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-793-170-20

  Query Match             92.7%;  Score 51;  DB 2;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 9
US-08-892-873-20/c
; Sequence 20, Application US/08892873
; Patent No. 6033908
;  GENERAL INFORMATION:
;    APPLICANT:  FALLAUX et al.
;    TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT
;    TITLE OF INVENTION:  ADENOVIRUS TO BE USED IN GENE THERAPY
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
;      STREET:  260 SHERIDAN AVENUE, PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/892,873
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/793,170
;      FILING DATE:  25-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO 97/00326
;      FILING DATE:  14-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201728.3
;      FILING DATE:  26-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201611.1
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.002.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-3377
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  55 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-892-873-20

  Query Match             92.7%;  Score 51;  DB 3;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db      55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 10
US-09-334-765A-20/c
; Sequence 20, Application US/09334765A
; Patent No. 6238893
; GENERAL INFORMATION:
;  APPLICANT:  Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO BE USED
;  TITLE OF INVENTION:  IN GENE THERAPY
;  FILE REFERENCE:  3833.2US
;  CURRENT APPLICATION NUMBER: US/09/334,765A
;  CURRENT FILING DATE:  1999-06-16
;  PRIOR APPLICATION NUMBER:  US 08/793,170
;  PRIOR FILING DATE:  1997-03-25
;  PRIOR APPLICATION NUMBER:  PCT/NL96/00244
;  PRIOR FILING DATE:  1996-06-14
;  PRIOR APPLICATION NUMBER:  EP 95201728.3
;  PRIOR FILING DATE:  1995-06-26
;  PRIOR APPLICATION NUMBER:  EP 95201611.1
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;  PRIOR FILING DATE:  1995-06-15
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  Corel WordPerfect 8.0
; SEQ ID NO 20
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: primer HP/cla2
US-09-334-765A-20

  Query Match             92.7%;  Score 51;  DB 4;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 11
US-09-356-575E-20/c
; Sequence 20, Application US/09356575E
; Patent No. 6265212
; GENERAL INFORMATION:
;  APPLICANT:  Fallaux, Frits
;  APPLICANT:  Hoeben, Robert
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  van der Eb, Alex
;  APPLICANT:  Schouten, Govert
;  TITLE OF INVENTION:  PACKAGING SYSTEMS
;  FILE REFERENCE:  2578-3935US
;  CURRENT APPLICATION NUMBER: US/09/356,575E
;  CURRENT FILING DATE:  1999-07-19
;  PRIOR APPLICATION NUMBER:  US 08/793,170
;  PRIOR FILING DATE:  1997-03-25
;  PRIOR APPLICATION NUMBER:  PCT/NL96/00244
;  PRIOR FILING DATE:  1996-06-14
;  PRIOR APPLICATION NUMBER:  EP 95201611.1
;  PRIOR FILING DATE:  1995-06-15
;  PRIOR APPLICATION NUMBER:  EP 95201728.3
;  PRIOR FILING DATE:  1995-06-26
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 20
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Derived from Adenovirus
US-09-356-575E-20

  Query Match             92.7%;  Score 51;  DB 4;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db     55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 12
US-09-333-820-20/c
; Sequence 20, Application US/09333820A
; Patent No. 6306652
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT: Hoeben, Robert C.
;  APPLICANT: Bout, Abraham
;  APPLICANT: Valerio, Domenico
;  APPLICANT: Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO BE USED
;  TITLE OF INVENTION: GENE THERAPY
;  FILE REFERENCE: 3833.1US
;  CURRENT APPLICATION NUMBER: US/09/333,820A
;  CURRENT FILING DATE: 1999-06-15
;  EARLIER APPLICATION NUMBER: US 08/793,170
;  EARLIER FILING DATE: 1997-03-25
;  EARLIER APPLICATION NUMBER: PCT/NL96/00244
;  EARLIER FILING DATE: 1996-06-14
;  EARLIER APPLICATION NUMBER: EP 95201728.3
;  EARLIER FILING DATE: 1995-06-26
;  EARLIER APPLICATION NUMBER: EP 95201611.1
;  EARLIER FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 20
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: primer HP/cla2
US-09-333-820-20

  Query Match             92.7%;  Score 51;  DB 4;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db     55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 13
US-09-358-036-42/c
; Sequence 42, Application US/09358036
; Patent No. 6340595
; GENERAL INFORMATION:
;  APPLICANT: Vogels, Ronald
;  APPLICANT: Bout, Abraham
;  APPLICANT: van Es, Helmuth
;  APPLICANT: Schouten, Govert
;  TITLE OF INVENTION: High Throughput Screening of Gene Function Using
;  TITLE OF INVENTION: Adenoviral Libraries for Functional Genomics
;  TITLE OF INVENTION: Applications
;  FILE REFERENCE: 21834108
;  CURRENT APPLICATION NUMBER: US/09/358,036
;  CURRENT FILING DATE: 1999-07-21
;  EARLIER APPLICATION NUMBER: US 09/097,239
;  EARLIER FILING DATE: 1995-07-25
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-358-036-42

  Query Match             92.7%;  Score 51;  DB 4;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 14
US-09-097-239-42/c
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; Sequence 42, Application US/09097239
; Patent No. 6413776
;  GENERAL INFORMATION:
;    APPLICANT:  VOGELS, RONALD,
;    APPLICANT:  BOUT, ABRAHAM,
;    APPLICANT:  VAN ES, HELMUTH HG,
;    APPLICANT:  SCHOUTEN, GOVERT
;    TITLE OF INVENTION:  HIGH THROUGHPUT SCREENING OF GENE
;    TITLE OF INVENTION:  FUNCTION USING ADENOVIRAL LIBRARIES FOR FUNCTIONAL
;    TITLE OF INVENTION:  GENOMICS APPLICATIONS
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/097,239
;      FILING DATE:  12-JUN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.008.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  55 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-09-097-239-42

  Query Match             92.7%;  Score 51;  DB 4;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 15
US-08-793-170-17
; Sequence 17, Application US/08793170
; Patent No. 5994128
;  GENERAL INFORMATION:
;    APPLICANT:  FALLAUX et al.
;    TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT
;    TITLE OF INVENTION:  ADENOVIRUS TO BE USED IN GENE THERAPY
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
;      STREET:  260 SHERIDAN AVENUE, PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,170
;      FILING DATE:  25-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO 97/00326
;      FILING DATE:  14-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201728.3
;      FILING DATE:  26-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201611.1
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.002.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-3377
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-793-170-17

  Query Match             86.2%;  Score 47.4;  DB 2;  Length 50;
  Best Local Similarity   98.0%;  Pred. No. 3.4e-08;
  Matches   48;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49
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Db       1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49


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Job time : 35 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 00:33:34 ; Search time 170.5 Seconds
(without alignments)
726.451 Million cell updates/sec

Title: US-09-918-029-19
Perfect score: 55
Sequence: 1 gtacattgacctagtgccgc.....gcggcactaggtcaatcgat 55

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	55	100.0	55	18	AAT48646	Synthetic haipin o
	2	55	100.0	55	21	AAZ59116	Oligonucleotide HP
	3	55	100.0	55	21	AAZ37959	Adenoviral constru
	4	55	100.0	55	22	AAF30232	Oligonucleotide fo
	5	55	100.0	55	24	ABK47032	Adenovirus vectro
c	6	51	92.7	55	18	AAT48647	Synthetic haipin o
c	7	51	92.7	55	21	AAZ59117	Oligonucleotide HP
c	8	51	92.7	55	24	ABK47033	Adenovirus vectro
	9	47.4	86.2	50	18	AAT48644	Synthetic haipin o
	10	47.4	86.2	50	22	AAF30231	Oligonucleotide fo
	11	47.4	86.2	50	24	ABK47030	Adenovirus vectro
	12	43.4	78.9	45	21	AAZ59131	Hairpin structure-
	13	43.4	78.9	45	21	AAZ37961	DNA molecule conta
	14	43.4	78.9	45	22	AAF30234	Oligonucleotide fo
	15	43.4	78.9	45	24	ABK47038	Adenovirus vector
c	16	43.4	78.9	50	18	AAT48645	Synthetic haipin o
c	17	43.4	78.9	50	21	AAZ37958	Adenoviral constru
c	18	43.4	78.9	50	24	ABK47031	Adenovirus vectro
	19	42.2	76.7	55	18	AAT48647	Synthetic haipin o
c	20	42.2	76.7	55	18	AAT48646	Synthetic haipin o
c	21	42.2	76.7	55	21	AAZ59116	Oligonucleotide HP
	22	42.2	76.7	55	21	AAZ59117	Oligonucleotide HP
c	23	42.2	76.7	55	21	AAZ37959	Adenoviral constru
c	24	42.2	76.7	55	22	AAF30232	Oligonucleotide fo
c	25	42.2	76.7	55	24	ABK47032	Adenovirus vectro
	26	42.2	76.7	55	24	ABK47033	Adenovirus vectro
c	27	39	70.9	54	21	AAZ37960	Adenoviral constru
c	28	38.6	70.2	50	18	AAT48644	Synthetic haipin o
	29	38.6	70.2	50	18	AAT48645	Synthetic haipin o
	30	38.6	70.2	50	21	AAZ37958	Adenoviral constru
c	31	38.6	70.2	50	22	AAF30231	Oligonucleotide fo
c	32	38.6	70.2	50	24	ABK47030	Adenovirus vectro
	33	38.6	70.2	50	24	ABK47031	Adenovirus vectro
	34	35.4	64.4	49	21	AAZ37957	Adenoviral constru
c	35	34.6	62.9	45	21	AAZ59131	Hairpin structure-
c	36	34.6	62.9	45	21	AAZ37961	DNA molecule conta
c	37	34.6	62.9	45	22	AAF30234	Oligonucleotide fo
c	38	34.6	62.9	45	24	ABK47038	Adenovirus vector
	39	30.2	54.9	54	21	AAZ37960	Adenoviral constru
c	40	26.6	48.4	49	21	AAZ37957	Adenoviral constru
	41	24.8	45.1	157	21	AAC11855	Human secreted pro
c	42	23.8	43.3	8384	22	AAK82907	Human immune/haema
c	43	23.6	42.9	63	24	ABL58790	AAV 5'ITR from vec
c	44	23.6	42.9	145	14	AAQ41448	AAV2 inverted term
c	45	23.6	42.9	145	16	AAT03385	Strict inverted te

ALIGNMENTS

RESULT 1
AAT48646
ID AAT48646 standard; DNA; 55 BP.
XX
AC AAT48646;
XX
DT 21-MAY-1997 (first entry)
XX
DE Synthetic haipin oligonucleotide HP/cla1.
XX
KW Gene therapy; vaccine; vector; adenovirus; packaging system;
KW hairpin; pICL; ss.
XX
OS Synthetic.
XX
PN WO9700326-A1.
XX
PD 03-JAN-1997.
XX
PF 14-JUN-1996; 96WO-NL00244.
XX
PR 26-JUN-1995; 95EP-0201728.
PR 15-JUN-1995; 95EP-0201611.
XX
PA (INTR-) INTROGENE BV.
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Bout A, Fallaux FJ, Hoeben RC, Valerio D, Van Der EBbAJ;
XX
DR WPI; 1997-077531/07.
XX
PT New packaging cells and nucleic acids for recombinant adenovirus -

PT have no overlapping sequences, prevents homologous recombination;
PT for use in gene therapy and vaccination
XX
PS Disclosure; Page 55; 88pp; English.
XX
CC Synthetic oligonucleotides HP/cla1 (AAT48646) and HP/cla2 (AAT48647)
CC were used to generate a synthetic hairpin. They contain a ClaI
CC recognition site to be used for hairpin formation. The
CC oligonucleotides were annealed and ligated into plasmid pCMV.TK,
CC at the adenovirus inverted terminal repeat, generating
CC pAd-CMV-hcTK. This plasmid was co-transfected with ClaI-digested
CC wild-type adenovirus 4 into 911 cells. A recombinant adenovirus
CC in which the CMV-hcTK expression cassette replaced the E1 sequences
CC was isolated.
XX
SQ Sequence 55 BP; 12 A; 17 C; 17 G; 9 T; 0 other;

Query Match 100.0%; Score 55; DB 18; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db 1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55

RESULT 2
AAZ59116
ID AAZ59116 standard; DNA; 55 BP.
XX
AC AAZ59116;
XX
DT 11-APR-2000 (first entry)
XX
DE Oligonucleotide HP/cla1 for generating hairpin structure.
XX
KW Expressible nucleic acid library; gene expression; gene function;
KW capillary formation; cell proliferation; hairpin structure; ss.
XX
OS Synthetic.
XX
PN WO9964582-A2.
XX
PD 16-DEC-1999.
XX
PF 11-JUN-1999; 99WO-NL00367.
XX
PR 12-JUN-1998; 98US-0097239.
XX
PA (INTR-) INTROGENE BV.
XX
PI Schouten G, Vogels R, Bout A, Van Es H;
XX
DR WPI; 2000-097536/08.
XX
PT New library of expressible nucleic acids, useful for high-throughput
PT screening of gene function, especially for identifying therapeutic
PT molecules -
XX
PS Example 3; Page 156; 223pp; English.
XX
CC The invention relates to a library of expressible nucleic acids (NA)
CC which contains many compartments, each comprising at least one vehicle
CC comprising at least one NA, the vehicle being capable of efficiently
CC introducing a NA into a cell for expression. The library is useful for
CC determining the function of one or more nucleic acids within the
CC library, or to screen for an expressible nucleic acid with a particular
CC desired function. It is especially useful for high throughput screening
CC of gene function for functional genomics applications and for screening
CC for nucleic acids with potential therapeutic value. Cell types
CC appropriate for selection of a particular phenotype may be useful for
CC capillary formation and cell proliferation. Oligonucleotides
CC AAZ59116-Z59117 were used to generate a hairpin structure in plasmid
CC pAd-CMV-hcTK. The hairpin structure was used to determine if it could be
CC used to prime reverse strand synthesis on the displaced strand after
CC replication initiation in the adenoviral inverted terminal repeat (ITR).
XX
SQ Sequence 55 BP; 12 A; 17 C; 17 G; 9 T; 0 other;

Query Match 100.0%; Score 55; DB 21; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db 1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55

RESULT 3
AAZ37959
ID AAZ37959 standard; DNA; 55 BP.
XX
AC AAZ37959;
XX
DT 07-FEB-2000 (first entry)
XX
DE Adenoviral construct generating primer Hp/cla1.
XX
KW Adenoviral vector; replication-defective; adenovirus; ITR; hepatitis;
KW inverted terminal repeat; encapsulation signal; gene therapy; tumor;
KW inherited disease; cystic fibrosis; Duchenne molecular dystrophy;
KW hypercholesterolemia; blood clotting disorder; hemophilia; restenosis;
KW autoimmune disease; rheumatoid arthritis; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9955132-A2.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-NL00235.
XX
PR 24-APR-1998; 98US-0065752.
XX
PA (INTR-) INTROGENE BV.
XX
PI Vogels R, Bout A;
XX
DR WPI; 2000-023229/02.
XX
PT New recombinant adenovirus vectors, used particularly for gene therapy
PT for treating inherited or acquired diseases -
XX
PS Disclosure; Page 118; 161pp; English.
XX
CC The invention provides methods of producing recombinant adenoviral
CC vectors (AdV's) for generating replication-defective adenoviruses.
CC Generating an AdV comprises fusing 2 partially overlapping sequences
CC nucleic acid molecules that are capable of combining with each other to
CC allow the generation of a physically linked nucleic acid comprising at
CC least 2 functional adenoviral inverted terminal repeats (ITRs), a
CC functional encapsulation signal and a nucleic acid of interest. The
CC products can be used for gene therapy for treating inherited diseases
CC e.g. cystic fibrosis, Duchenne molecular dystrophy,
CC hypercholesterolemia, blood clotting disorders (hemophilia) or acquired
CC diseases such as tumors, hepatitis, (auto)immune diseases, restenosis, or
CC rheumatoid arthritis. Sequences AAZ37954-960 represent primers used for
CC PCR amplification of DNA fragments used for generation of adenoviral
CC constructs of the invention.
XX
SQ Sequence 55 BP; 12 A; 17 C; 17 G; 9 T; 0 other;

Query Match 100.0%; Score 55; DB 21; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
```

RESULT 4
AAF30232
ID AAF30232 standard; DNA; 55 BP.
XX
AC AAF30232;
XX
DT 30-APR-2001 (first entry)
XX
DE Oligonucleotide forming hairpin structure.
XX
KW Adenovirus; vector; gene therapy; packaging cell; hairpin; ds.
XX
OS *Synthetic*.
XX
FH Key Location/Qualifiers
FT misc_feature 1..4
FT /*tag= a
FT /note= "single-stranded 5' overhang"
FT misc_feature 55
FT /*tag= b
FT /note= "single-stranded overhang on complementary
FT strand of sequence 5'-GTAC-3"
XX
PN WO200105945-A2.
XX
PD 25-JAN-2001.
XX
PF 19-JUL-2000; 2000WO-EP07074.
XX
PR 19-JUL-1999; 99US-0356575.
XX
PA (INTR-) INTROGENE BV.
XX
PI *Hoeben RC*, *Bout A*, *Valerio D*, *Van Der Eb AJ*, Schouten G;
PI Fallaux FJ;
XX
DR WPI; 2001-147334/15.
XX
PT Producing recombinant adenovirus for use in gene therapy, comprises
PT culturing cells containing adenoviral nucleic acid having an
PT *encapsidating signal and inverted terminal repeat*, and lacking
PT overlapping sequences -
XX
PS Example; Page 39; 97pp; English.
XX
CC The present sequence is that of an oligonucleotide formed from 2
CC partially complementary oligonucleotides creating a hairpin
CC structure. The oligonucleotide forms an ClaI recognition site
CC when inserted into the ClaI site of plasmid pICL (see AAF30233).
CC This was performed as part of an experiment to determine whether
CC the hairpin could be used as a primer for reverse strand synthesis
CC on the displaced strand after replication had started from the
CC inverted terminal repeat (ITR) of the vector. In adenovirus
CC infected cells, linear DNA fragments have on one terminus an
CC *adenovirus-derived* ITR and at the other terminus a sequence that
CC can anneal to the same strand, when present in single-stranded
CC form, thereby generating a hairpin structure, and will be
CC converted to structures with ITRs at both ends. The resulting DNA
CC molecules will replicate by the same mechanism as the wild-type
CC adenovirus genomes. The invention provides adenovirus vectors and
CC packaging cell lines useful in the safe generation of E1-deleted
CC recombinant adenovirus vectors for gene therapy applications.
CC Packaging cells contain adenovirus nucleic acids having an
CC encapsidating signal and ITR, but lack sequences that overlap with
CC the vector, thereby preventing homologous recombination.
XX
SQ Sequence 55 BP; 12 A; 17 C; 17 G; 9 T; 0 other;

```
  Query Match           100.0%;  Score 55;  DB 22;  Length 55;
  Best Local Similarity 100.0%;  Pred. No. 1.3e-10;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
```

RESULT 5
ABK47032
ID ABK47032 standard; DNA; 55 BP.
XX
AC ABK47032;
XX
DT 05-JUN-2002 (first entry)
XX
DE Adenovirus vectro pICLhac/haw hairpin linker sequence Hp/clal#1.
XX
KW Adenovirus vector library; ss; linker; high throughput screening;
KW RCA; replication competent adenovirus.
XX
OS Synthetic.
XX
PN US6340595-B1.
XX
PD 22-JAN-2002.
XX
PF 21-JUL-1999; 99US-0358036.
XX
PR 12-JUN-1998; 98US-0097239.
XX
PA (GALA-) GALAPAGOS GENOMICS NV.
XX
PI Vogels R, Bout A, Van Es H, Schouten G;
XX
DR WPI; 2002-224926/28.
XX
PT Library of expressible nucleic acids, useful for determining nucleic
PT acid function, comprises one or more *adenoviral vectors* capable of
PT transfecting a host cell with the nucleic acid -
XX
PS Example 3; Column 85; 111pp; English.
XX
CC The invention relates to a library (I) of a multitude of unique
CC expressible nucleic acids (NA), comprises a number of compartments
CC (II), each consisting of one or more adenoviral *vectors (III)*
CC comprising at least one unique NA of (I) in an aqueous medium, where
CC (III) is capable of introducing the NA into a host cell (IV), is
CC capable of expressing the product of the NA in (IV), and is deleted in
CC a portion of the adenoviral genome necessary for replication. Also
CC included is a method for producing the library. The library is useful for
CC determining the function of at least one nucleic acid that is present.
CC The library uses high throughput *generation of recombinant* adenoviral
CC vector libraries containing one or more sample nucleic acids, followed by
CC high throughput screening of the adenoviral vector libraries in a host to
CC alter the phenotype of the host as a means of assigning a function to
CC expression product(s) of the sample nucleic acids. The entire process
CC lends itself to automation especially when implemented in a 96-well or
CC other multi-well format. The high throughput screening, using a number of
CC different in vitro assays, provides a *means of efficiently obtaining*
CC functional information in a relatively short period of time. The
CC member(s) of the recombinant adenoviral libraries that exhibit or induce
CC a desired phenotype in a host in vitro or in situ are identified to
CC reduce the libraries to a manageable number of recombinant adenoviral
CC vectors or clones which can be tested in vitro in an animal model.
CC Furthermore, the methods produce RCA-free adenoviral libraries. RCA
CC (replication competent adenovirus) *contamination throughout the libraries*
CC could become a major obstacle, especially if libraries are continuously
CC amplified for use in multiple screening programs. Additionally, a further
CC advantage is minimisation of the number of steps involved in the process.
CC There is no requirement for cloning each individual adenovirus before use
CC in a high throughput screening program. Other systems include one or more

```
CC   steps in E. coli to achieve homologous recombination for the various
CC   adenoviral plasmids necessary for vector generation. The present
CC   sequence is a linker sequence used in the construction of the adenoviral
CC   vector library of the invention.
XX
SQ   Sequence 55 BP; 12 A; 17 C; 17 G; 9 T; 0 other;

  Query Match             100.0%;  Score 55;  DB 24;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-10;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55


RESULT 6
AAT48647/c
ID   AAT48647 standard; DNA; 55 BP.
XX
AC   AAT48647;
XX
DT   21-MAY-1997  (first entry)
XX
DE   Synthetic haipin oligonucleotide HP/cla2.
XX
KW   Gene therapy; vaccine; vector; adenovirus; packaging system;
KW   hairpin; pICL; ss.
XX
OS   Synthetic.
XX
PN   WO9700326-A1.
XX
PD   03-JAN-1997.
XX
PF   14-JUN-1996;   96WO-NL00244.
XX
PR   26-JUN-1995;   95EP-0201728.
PR   15-JUN-1995;   95EP-0201611.
XX
PA   (INTR-) INTROGENE BV.
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Bout A,  Fallaux FJ,  Hoeben RC,  Valerio D,  Van Der EBbAJ;
XX
DR   WPI; 1997-077531/07.
XX
PT   New packaging cells and nucleic acids for recombinant adenovirus -
PT   have no overlapping sequences, prevents homologous recombination;
PT   for use in gene therapy and vaccination
XX
PS   Disclosure; Page 55; 88pp; English.
XX
CC   Synthetic oligonucleotides HP/cla1 (AAT48646) and HP/cla2 (AAT48647)
CC   were used to generate a synthetic hairpin.  They contain a ClaI
CC   recognition site to be used for hairpin formation.  The
CC   oligonucleotides were annealed and ligated into plasmid pCMV.TK,
CC   at the adenovirus inverted terminal repeat, generating
CC   pAd-CMV-hcTK.  This plasmid was co-transfected with ClaI-digested
CC   wild-type adenovirus 4 into 911 cells.  A recombinant adenovirus
CC   in which the CMV-hcTK expression cassette replaced the E1 sequences
CC   was isolated.
XX
SQ   Sequence 55 BP; 9 A; 17 C; 17 G; 12 T; 0 other;

  Query Match             92.7%;  Score 51;  DB 18;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 7
AAZ59117/c
ID   AAZ59117 standard; DNA; 55 BP.
XX
AC   AAZ59117;
XX
DT   11-APR-2000  (first entry)
XX
DE   Oligonucleotide HP/cla2 for generating hairpin structure.
XX
KW   Expressible nucleic acid library; gene expression; gene function;
KW   capillary formation; cell proliferation; hairpin structure; ss.
XX
OS   Synthetic.
XX
PN   WO9964582-A2.
XX
PD   16-DEC-1999.
XX
PF   11-JUN-1999;   99WO-NL00367.
XX
PR   12-JUN-1998;   98US-0097239.
XX
PA   (INTR-) INTROGENE BV.
XX
PI   Schouten G,  Vogels R,  Bout A,  Van Es H;
XX
DR   WPI; 2000-097536/08.
XX
PT   New library of expressible nucleic acids, useful for high-throughput
PT   screening of gene function, especially for identifying therapeutic
PT   molecules -
XX
PS   Example 3; Page 156; 223pp; English.
XX
CC   The invention relates to a library of expressible nucleic acids (NA)
CC   which contains many compartments, each comprising at least one vehicle
CC   comprising at least one NA, the vehicle being capable of efficiently
CC   introducing a NA into a cell for expression. The library is useful for
CC   determining the function of one or more nucleic acids within the
CC   library, or to screen for an expressible nucleic acid with a particular
CC   desired function. It is especially useful for high throughput screening
CC   of gene function for functional genomics applications and for screening
CC   for nucleic acids with potential therapeutic value. Cell types
CC   appropriate for selection of a particular phenotype may be useful for
CC   capillary formation and cell proliferation.  Oligonucleotides
CC   AAZ59116-Z59117 were used to generate a hairpin structure in plasmid
CC   pAd-CMV-hcTK. The hairpin structure was used to determine if it could be
CC   used to prime reverse strand synthesis on the displaced strand after
CC   replication initiation in the adenoviral inverted terminal repeat (ITR).
XX
SQ   Sequence 55 BP; 9 A; 17 C; 17 G; 12 T; 0 other;

  Query Match             92.7%;  Score 51;  DB 21;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 8
ABK47033/c
ID   ABK47033 standard; DNA; 55 BP.
XX
AC   ABK47033;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Adenovirus vectro pICLhac/haw hairpin linker sequence Hp/cla1#2.
XX
```

KW Adenovirus vector library; ss; linker; high throughput screening;
KW RCA; replication competent adenovirus.
XX
OS Synthetic.
XX
PN US6340595-B1.
XX
PD 22-JAN-2002.
XX
PF 21-JUL-1999; 99US-0358036.
XX
PR 12-JUN-1998; 98US-0097239.
XX
PA (GALA-) GALAPAGOS GENOMICS NV.
XX
PI Vogels R, Bout A, Van Es H, Schouten G;
XX
DR WPI; 2002-224926/28.
XX
PT Library of expressible nucleic acids, useful for determining nucleic
PT acid function, comprises one or more adenoviral vectors capable of
PT transfecting a host cell with the nucleic acid -
XX
PS Example 3; Column 85; 111pp; English.
XX
CC The invention relates to a library (I) of a multitude of unique
CC expressible nucleic acids (NA), comprises a number of compartments
CC (II), each consisting of one or more adenoviral vectors (III)
CC comprising at least one unique NA of (I) in an aqueous medium, where
CC (III) is capable of introducing the NA into a host cell (IV), is
CC capable of expressing the product of the NA in (IV), and is deleted in
CC a portion of the adenoviral genome necessary for replication. Also
CC included is a method for producing the library. The library is useful for
CC determining the function of at least one nucleic acid that is present.
CC The library uses high throughput generation of recombinant adenoviral
CC vector libraries containing one or more sample nucleic acids, followed by
CC high throughput screening of the adenoviral vector libraries in a host to
CC alter the phenotype of the host as a means of assigning a function to
CC expression product(s) of the sample nucleic acids. The entire process
CC lends itself to automation especially when implemented in a 96-well or
CC other multi-well format. The high throughput screening, using a number of
CC different in vitro assays, provides a means of efficiently obtaining
CC functional information in a relatively short period of time. The
CC member(s) of the recombinant adenoviral libraries that exhibit or induce
CC a desired phenotype in a host in vitro or in situ are identified to
CC reduce the libraries to a manageable number of recombinant adenoviral
CC vectors or clones which can be tested in vitro in an animal model.
CC Furthermore, the methods produce RCA-free adenoviral libraries. RCA
CC (replication competent adenovirus) contamination throughout the libraries
CC could become a major obstacle, especially if libraries are continuously
CC amplified for use in multiple screening programs. Additionally, a further
CC advantage is minimisation of the number of steps involved in the process.
CC There is no requirement for cloning each individual adenovirus before use
CC in a high throughput screening program. Other systems include one or more
CC steps in E. coli to achieve homologous recombination for the various
CC adenoviral plasmids necessary for vector generation. The present
CC sequence is a linker sequence used in the construction of the adenoviral
CC vector library of the invention.
XX
SQ Sequence 55 BP; 9 A; 17 C; 17 G; 12 T; 0 other;

Query Match 92.7%; Score 51; DB 24; Length 55;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5
```

RESULT 9
AAT48644
ID AAT48644 standard; DNA; 50 BP.
XX
AC AAT48644;
XX
DT 21-MAY-1997 (first entry)
XX
DE Synthetic haipin oligonucleotide HP/asp1.
XX
KW Gene therapy; vaccine; vector; adenovirus; packaging system;
KW hairpin; pICL; ss.
XX
OS Synthetic.
XX
PN WO9700326-A1.
XX
PD 03-JAN-1997.
XX
PF 14-JUN-1996; 96WO-NL00244.
XX
PR 26-JUN-1995; 95EP-0201728.
PR 15-JUN-1995; 95EP-0201611.
XX
PA (INTR-) INTROGENE BV.
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Bout A, Fallaux FJ, Hoeben RC, Valerio D, Van Der EBbAJ;
XX
DR WPI; 1997-077531/07.
XX
PT New packaging cells and nucleic acids for recombinant adenovirus -
PT have no overlapping sequences, prevents homologous recombination;
PT for use in gene therapy and vaccination
XX
PS Disclosure; Page 55; 88pp; English.
XX
CC Synthetic oligonucleotides HP/asp1 (AAT48644) and HP/asp2 (AAT48645)
CC were used to generate a synthetic hairpin, recreating an Asp718
CC site at one of the termini if inserted in the Asp718 site of
CC adenovirus minimal vector pICL (see also AAT48630). Insertion of
CC the oligonucleotides into pICL generated clone pICLhac (correct
CC orientation) and pICLhaw (reverse, non-functional orientation).
CC The constructs were used to demonstrate the competence of a
CC synthetic DNA sequence, that is capable of forming a hairpin
CC structure, to serve as a primer for reverse strand synthesis in
CC the generation of double-stranded DNA molecules in cells that
CC contain and express adenovirus genes.
XX
SQ Sequence 50 BP; 10 A; 17 C; 17 G; 6 T; 0 other;

Query Match 86.2%; Score 47.4; DB 18; Length 50;
Best Local Similarity 98.0%; Pred. No. 7.1e-08;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49
           ||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49
```

RESULT 10
AAF30231
ID AAF30231 standard; DNA; 50 BP.
XX
AC AAF30231;
XX
DT 30-APR-2001 (first entry)
XX
DE Oligonucleotide forming hairpin structure.
XX
KW Adenovirus; vector; gene therapy; packaging cell; hairpin; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..4

```
FT                   /*tag=  a
FT                   /note= "single-stranded 5' overhang"
FT   misc_feature    50
FT                   /*tag=  b
FT                   /note= "single-stranded overhang on complementary
FT                          strand of sequence 5'-GTAC-3"
XX
PN   WO200105945-A2.
XX
PD   25-JAN-2001.
XX
PF   19-JUL-2000; 2000WO-EP07074.
XX
PR   19-JUL-1999;   99US-0356575.
XX
PA   (INTR-) INTROGENE BV.
XX
PI   Hoeben RC,  Bout A,  Valerio D,  Van Der Eb AJ,  Schouten G;
PI   Fallaux FJ;
XX
DR   WPI; 2001-147334/15.
XX
PT   Producing recombinant adenovirus for use in gene therapy, comprises
PT   culturing cells containing adenoviral nucleic acid having an
PT   encapsidating signal and inverted terminal repeat, and lacking
PT   overlapping sequences -
XX
PS   Example; Page 39; 97pp; English.
XX
CC   The present sequence is that of an oligonucleotide formed from 2
CC   partially complementary oligonucleotides creating a hairpin
CC   structure.  The oligonucleotide forms an Asp718 recognition site
CC   when inserted into the Asp718 site of plasmid pICL (see AAF30233).
CC   This was performed as part of an experiment to determine whether
CC   the hairpin could be used as a primer for reverse strand synthesis
CC   on the displaced strand after replication had started from the
CC   inverted terminal repeat (ITR) of the vector.  In adenovirus
CC   infected cells, linear DNA fragments have on one terminus an
CC   adenovirus-derived ITR and at the other terminus a sequence that
CC   can anneal to the same strand, when present in single-stranded
CC   form, thereby generating a hairpin structure, and will be
CC   converted to structures with ITRs at both ends.  The resulting DNA
CC   molecules will replicate by the same mechanism as the wild-type
CC   adenovirus genomes.  The invention provides adenovirus vectors and
CC   packaging cell lines useful in the safe generation of E1-deleted
CC   recombinant adenovirus vectors for gene therapy applications.
CC   Packaging cells contain adenovirus nucleic acids having an
CC   encapsidating signal and ITR, but lack sequences that overlap with
CC   the vector, thereby preventing homologous recombination.
XX
SQ   Sequence 50 BP; 10 A; 17 C; 17 G; 6 T; 0 other;

  Query Match             86.2%;  Score 47.4;  DB 22;  Length 50;
  Best Local Similarity   98.0%;  Pred. No. 7.1e-08;
  Matches   48;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49
           ||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49


RESULT 11
ABK47030
ID   ABK47030 standard; DNA; 50 BP.
XX
AC   ABK47030;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Adenovirus vectro pICLhac/haw linker sequence Hp/asp1#1.
XX
KW   Adenovirus vector library; ss; linker; high throughput screening;
KW   RCA; replication competent adenovirus.
XX
OS   Synthetic.
XX
PN   US6340595-B1.
XX
PD   22-JAN-2002.
XX
PF   21-JUL-1999;   99US-0358036.
XX
PR   12-JUN-1998;   98US-0097239.
XX
PA   (GALA-) GALAPAGOS GENOMICS NV.
XX
PI   Vogels R,  Bout A,  Van Es H,  Schouten G;
XX
DR   WPI; 2002-224926/28.
XX
PT   Library of expressible nucleic acids, useful for determining nucleic
PT   acid function, comprises one or more adenoviral vectors capable of
PT   transfecting a host cell with the nucleic acid -
XX
PS   Example 3; Column 84; 111pp; English.
XX
CC   The invention relates to a library (I) of a multitude of unique
CC   expressible nucleic acids (NA), comprises a number of compartments
CC   (II), each consisting of one or more adenoviral vectors (III)
CC   comprising at least one unique NA of (I) in an aqueous medium, where
CC   (III) is capable of introducing the NA into a host cell (IV), is
CC   capable of expressing the product of the NA in (IV), and is deleted in
CC   a portion of the adenoviral genome necessary for replication. Also
CC   included is a method for producing the library. The library is useful for
CC   determining the function of at least one nucleic acid that is present.
CC   The library uses high throughput generation of recombinant adenoviral
CC   vector libraries containing one or more sample nucleic acids, followed by
CC   high throughput screening of the adenoviral vector libraries in a host to
CC   alter the phenotype of the host as a means of assigning a function to
CC   expression product(s) of the sample nucleic acids. The entire process
CC   lends itself to automation especially when implemented in a 96-well or
CC   other multi-well format. The high throughput screening, using a number of
CC   different in vitro assays, provides a means of efficiently obtaining
CC   functional information in a relatively short period of time. The
CC   member(s) of the recombinant adenoviral libraries that exhibit or induce
CC   a desired phenotype in a host in vitro or in situ are identified to
CC   reduce the libraries to a manageable number of recombinant adenoviral
CC   vectors or clones which can be tested in vitro in an animal model.
CC   Furthermore, the methods produce RCA-free adenoviral libraries. RCA
CC   (replication competent adenovirus) contamination throughout the libraries
CC   could become a major obstacle, especially if libraries are continuously
CC   amplified for use in multiple screening programs. Additionally, a further
CC   advantage is minimisation of the number of steps involved in the process.
CC   There is no requirement for cloning each individual adenovirus before use
CC   in a high throughput screening program. Other systems include one or more
CC   steps in E. coli to achieve homologous recombination for the various
CC   adenoviral plasmids necessary for vector generation. The present
CC   sequence is a linker sequence used in the construction of the adenoviral
CC   vector library of the invention.
XX
SQ   Sequence 50 BP; 10 A; 17 C; 17 G; 6 T; 0 other;

  Query Match             86.2%;  Score 47.4;  DB 24;  Length 50;
  Best Local Similarity   98.0%;  Pred. No. 7.1e-08;
  Matches   48;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49
           ||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49


RESULT 12
AAZ59131
ID   AAZ59131 standard; DNA; 45 BP.
XX
AC   AAZ59131;
```

XX
DT 11-APR-2000 (first entry)
XX
DE Hairpin structure-forming oligonucleotide.
XX
KW Expressible nucleic acid library; gene expression; gene function;
KW capillary formation; cell proliferation; hairpin structure; ss.
XX
OS Synthetic.
XX
PN WO9964582-A2.
XX
PD 16-DEC-1999.
XX
PF 11-JUN-1999; 99WO-NL00367.
XX
PR 12-JUN-1998; 98US-0097239.
XX
PA (INTR-) INTROGENE BV.
XX
PI Schouten G, Vogels R, Bout A, Van Es H;
XX
DR WPI; 2000-097536/08.
XX
PT New library of expressible nucleic acids, useful for high-throughput
PT screening of gene function, especially for identifying therapeutic
PT molecules -
XX
PS Disclosure; Fig 15; 223pp; English.
XX
CC The invention relates to a library of expressible nucleic acids (NA)
CC which contains many compartments, each comprising at least one vehicle
CC comprising at least one NA, the vehicle being capable of efficiently
CC introducing a NA into a cell for expression. The library is useful for
CC determining the function of one or more nucleic acids within the library,
CC or to screen for an expressible nucleic acid with a particular desired
CC function. It is especially useful for high throughput screening of gene
CC function for functional genomics applications and for screening for
CC nucleic acids with potential therapeutic value. Cell types appropriate
CC for selection of a particular phenotype may be useful for capillary
CC formation and cell proliferation. This oligonucleotides is used to
CC generate a hairpin structure which was used to determine if it could be
CC used to prime reverse strand synthesis on the displaced strand after
CC replication initiation in the adenoviral inverted terminal repeat (ITR).
XX
SQ Sequence 45 BP; 9 A; 16 C; 15 G; 5 T; 0 other;

Query Match 78.9%; Score 43.4; DB 21; Length 45;
Best Local Similarity 97.8%; Pred. No. 1.9e-06;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAG 45
```

RESULT 13
AAZ37961
ID AAZ37961 standard; DNA; 45 BP.
XX
AC AAZ37961;
XX
DT 07-FEB-2000 (first entry)
XX
DE DNA molecule containing Hp/asp sequences.
XX
KW Adenoviral vector; replication-defective; adenovirus; ITR; hepatitis;
KW inverted terminal repeat; encapsulation signal; gene therapy; tumor;
KW inherited disease; cystic fibrosis; Duchenne molecular dystrophy;
KW hypercholesterolemia; blood clotting disorder; hemophilia; restenosis;
KW autoimmune disease; rheumatoid arthritis; ss.
XX
OS Synthetic.
XX
PN WO9955132-A2.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-NL00235.
XX
PR 24-APR-1998; 98US-0065752.
XX
PA (INTR-) INTROGENE BV.
XX
PI Vogels R, Bout A;
XX
DR WPI; 2000-023229/02.
XX
PT New recombinant adenovirus vectors, used particularly for gene therapy
PT for treating inherited or acquired diseases -
XX
PS Disclosure; Fig 15; 161pp; English.
XX
CC The invention provides methods of producing recombinant adenoviral
CC vectors (AdV's) for generating replication-defective adenoviruses.
CC Generating an AdV comprises fusing 2 partially overlapping sequences
CC nucleic acid molecules that are capable of combining with each other to
CC allow the generation of a physically linked nucleic acid comprising at
CC least 2 functional adenoviral inverted terminal repeats (ITRs), a
CC functional encapsulation signal and a nucleic acid of interest. The
CC products can be used for gene therapy for treating inherited diseases
CC e.g. cystic fibrosis, Duchenne molecular dystrophy, hypercholesterolemia,
CC blood clotting disorders (hemophilia) or acquired diseases such as
CC tumors, hepatitis, (auto)immune diseases, restenosis, or rheumatoid
CC arthritis.
XX
SQ Sequence 45 BP; 9 A; 16 C; 15 G; 5 T; 0 other;

Query Match 78.9%; Score 43.4; DB 21; Length 45;
Best Local Similarity 97.8%; Pred. No. 1.9e-06;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAG 45
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RESULT 14
AAF30234
ID AAF30234 standard; DNA; 45 BP.
XX
AC AAF30234;
XX
DT 30-APR-2001 (first entry)
XX
DE Oligonucleotide forming hairpin structure.
XX
KW Adenovirus; vector; gene therapy; packaging cell; hairpin; ss.
XX
OS Synthetic.
XX
PN WO200105945-A2.
XX
PD 25-JAN-2001.
XX
PF 19-JUL-2000; 2000WO-EP07074.
XX
PR 19-JUL-1999; 99US-0356575.
XX
PA (INTR-) INTROGENE BV.
XX
PI Hoeben RC, Bout A, Valerio D, Van Der Eb AJ, Schouten G;
PI Fallaux FJ;
XX
DR WPI; 2001-147334/15.
XX

```
PT   Producing recombinant adenovirus for use in gene therapy, comprises
PT   culturing cells containing adenoviral nucleic acid having an
PT   encapsidating signal and inverted terminal repeat, and lacking
PT   overlapping sequences -
XX
PS   Example; Page 53; 97pp; English.
XX
CC   The present sequence is that of an oligonucleotide that forms a
CC   hairpin structure. The oligonucleotide creates an Asp718 recognition
CC   site when inserted into the Asp718 site of plasmid pICL (see
CC   AAF30233). This was performed as part of an experiment to determine
CC   whether the hairpin could be used as a primer for reverse strand
CC   synthesis on the displaced strand after replication had started from
CC   the inverted terminal repeat (ITR) of the vector. In adenovirus
CC   infected cells, linear DNA fragments have on one terminus an
CC   adenovirus-derived ITR and at the other terminus a sequence that
CC   can anneal to the same strand, when present in single-stranded
CC   form, thereby generating a hairpin structure, and will be
CC   converted to structures with ITRs at both ends. The resulting DNA
CC   molecules will replicate by the same mechanism as the wild-type
CC   adenovirus genomes. The invention provides adenovirus vectors and
CC   packaging cell lines useful in the safe generation of E1-deleted
CC   recombinant adenovirus vectors for gene therapy applications.
CC   Packaging cells contain adenovirus nucleic acids having an
CC   encapsidating signal and ITR, but lack sequences that overlap with
CC   the vector, thereby preventing homologous recombination.
XX
SQ   Sequence 45 BP; 9 A; 16 C; 15 G; 5 T; 0 other;

  Query Match             78.9%;  Score 43.4;  DB 22;  Length 45;
  Best Local Similarity   97.8%;  Pred. No. 1.9e-06;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAG 45
           ||||| |||||||||||||||||||||||||||||||||||||||
Db       1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAG 45


RESULT 15
ABK47038
ID   ABK47038 standard; DNA; 45 BP.
XX
AC   ABK47038;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Adenovirus vector potential hairpin forming sequence.
XX
KW   Adenovirus vector library; ss; high throughput screening; ASp7181;
KW   RCA; replication competent adenovirus; hairpin; pICLHa.
XX
OS   Mastadenovirus Ad5.
XX
PN   US6340595-B1.
XX
PD   22-JAN-2002.
XX
PF   21-JUL-1999;   99US-0358036.
XX
PR   12-JUN-1998;   98US-0097239.
XX
PA   (GALA-) GALAPAGOS GENOMICS NV.
XX
PI   Vogels R, Bout A, Van Es H, Schouten G;
XX
DR   WPI; 2002-224926/28.
XX
PT   Library of expressible nucleic acids, useful for determining nucleic
PT   acid function, comprises one or more adenoviral vectors capable of
PT   transfecting a host cell with the nucleic acid -
XX
PS   Example 3; Fig 15; 111pp; English.
XX
CC   The invention relates to a library (I) of a multitude of unique
CC   expressible nucleic acids (NA), comprises a number of compartments
CC   (II), each consisting of one or more adenoviral vectors (III)
CC   comprising at least one unique NA of (I) in an aqueous medium, where
CC   (III) is capable of introducing the NA into a host cell (IV), is
CC   capable of expressing the product of the NA in (IV), and is deleted in
CC   a portion of the adenoviral genome necessary for replication. Also
CC   included is a method for producing the library. The library is useful for
CC   determining the function of at least one nucleic acid that is present.
CC   The library uses high throughput generation of recombinant adenoviral
CC   vector libraries containing one or more sample nucleic acids, followed by
CC   high throughput screening of the adenoviral vector libraries in a host to
CC   alter the phenotype of the host as a means of assigning a function to
CC   expression product(s) of the sample nucleic acids. The entire process
CC   lends itself to automation especially when implemented in a 96-well or
CC   other multi-well format. The high throughput screening, using a number of
CC   different in vitro assays, provides a means of efficiently obtaining
CC   functional information in a relatively short period of time. The
CC   member(s) of the recombinant adenoviral libraries that exhibit or induce
CC   a desired phenotype in a host in vitro or in situ are identified to
CC   reduce the libraries to a manageable number of recombinant adenoviral
CC   vectors or clones which can be tested in vitro in an animal model.
CC   Furthermore, the methods produce RCA-free adenoviral libraries. RCA
CC   (replication competent adenovirus) contamination throughout the libraries
CC   could become a major obstacle, especially if libraries are continuously
CC   amplified for use in multiple screening programs. Additionally, a further
CC   advantage is minimisation of the number of steps involved in the process.
CC   There is no requirement for cloning each individual adenovirus before use
CC   in a high throughput screening program. Other systems include one or more
CC   steps in E. coli to achieve homologous recombination for the various
CC   adenoviral plasmids necessary for vector generation. The present
CC   sequence is part of the adenovirus vector pICLHa which can form a
CC   hairpin sequence on digestion with restriction endonuclease Asp7181.
CC   During chain elongation, the free 3' terminus becomes displaced and can
CC   acts as a double-stranded template for cellular or viral DNA polymerase.
XX
SQ   Sequence 45 BP; 9 A; 16 C; 15 G; 5 T; 0 other;

  Query Match             78.9%;  Score 43.4;  DB 24;  Length 45;
  Best Local Similarity   97.8%;  Pred. No. 1.9e-06;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAG 45
           ||||| |||||||||||||||||||||||||||||||||||||||
Db       1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAG 45


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Job time : 172.5 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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Title: US-09-918-029-19
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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1: gb_ba:*
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33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		55	100.0	55	6	AR091516	AR091516 Sequence
2		55	100.0	55	6	AR154396	AR154396 Sequence
3		55	100.0	55	6	AR174324	AR174324 Sequence
4		55	100.0	55	6	AR183308	AR183308 Sequence
5		55	100.0	55	6	AX080360	AX080360 Sequence
6	c	51	92.7	55	6	AR091517	AR091517 Sequence
7	c	51	92.7	55	6	AR154397	AR154397 Sequence
8	c	51	92.7	55	6	AR174325	AR174325 Sequence
9	c	51	92.7	55	6	AR183309	AR183309 Sequence
10	c	51	92.7	55	6	AX080361	AX080361 Sequence
11		47.4	86.2	50	6	AR091514	AR091514 Sequence
12		47.4	86.2	50	6	AR154394	AR154394 Sequence
13		47.4	86.2	50	6	AR174322	AR174322 Sequence
14		47.4	86.2	50	6	AR183306	AR183306 Sequence
15		47.4	86.2	50	6	AX080358	AX080358 Sequence
16		43.4	78.9	45	6	AR091519	AR091519 Sequence
17		43.4	78.9	45	6	AR154399	AR154399 Sequence
18		43.4	78.9	45	6	AR174327	AR174327 Sequence
19		43.4	78.9	45	6	AR183314	AR183314 Sequence
20	c	43.4	78.9	50	6	AR091515	AR091515 Sequence
21	c	43.4	78.9	50	6	AR154395	AR154395 Sequence
22	c	43.4	78.9	50	6	AR174323	AR174323 Sequence
23	c	43.4	78.9	50	6	AR183307	AR183307 Sequence
24	c	43.4	78.9	50	6	AX080359	AX080359 Sequence
25	c	42.2	76.7	55	6	AR091516	AR091516 Sequence
26		42.2	76.7	55	6	AR091517	AR091517 Sequence
27	c	42.2	76.7	55	6	AR154396	AR154396 Sequence
28		42.2	76.7	55	6	AR154397	AR154397 Sequence
29	c	42.2	76.7	55	6	AR174324	AR174324 Sequence
30		42.2	76.7	55	6	AR174325	AR174325 Sequence
31	c	42.2	76.7	55	6	AR183308	AR183308 Sequence
32		42.2	76.7	55	6	AR183309	AR183309 Sequence
33	c	42.2	76.7	55	6	AX080360	AX080360 Sequence
34		42.2	76.7	55	6	AX080361	AX080361 Sequence
35		40.2	73.1	45	6	AX080363	AX080363 Sequence
36	c	38.6	70.2	50	6	AR091514	AR091514 Sequence
37		38.6	70.2	50	6	AR091515	AR091515 Sequence
38	c	38.6	70.2	50	6	AR154394	AR154394 Sequence
39		38.6	70.2	50	6	AR154395	AR154395 Sequence
40	c	38.6	70.2	50	6	AR174322	AR174322 Sequence
41		38.6	70.2	50	6	AR174323	AR174323 Sequence
42	c	38.6	70.2	50	6	AR183306	AR183306 Sequence
43		38.6	70.2	50	6	AR183307	AR183307 Sequence
44	c	38.6	70.2	50	6	AX080358	AX080358 Sequence
45		38.6	70.2	50	6	AX080359	AX080359 Sequence

ALIGNMENTS

RESULT 1
AR091516
LOCUS AR091516 55 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 19 from patent US 5994128.
ACCESSION AR091516
VERSION AR091516.1 GI:10018271
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 55)
AUTHORS Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van der Eb,A.Jan., Bout,A. and Valerio,D.
TITLE Packaging systems for human recombinant adenovirus to be used in gene therapy

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  JOURNAL   Patent: US 5994128-A 19 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT       12 a      17 c      17 g       9 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.7e-08;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55


RESULT 2
AR154396
LOCUS       AR154396                 55 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 19 from patent US 6238893.
ACCESSION   AR154396
VERSION     AR154396.1  GI:15122449
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Hoeben,R.Cornelis. and Bout,A.
  TITLE     Method for intracellular DNA amplification
  JOURNAL   Patent: US 6238893-A 19 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT       12 a      17 c      17 g       9 t
ORIGIN

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Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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RESULT 3
AR174324
LOCUS       AR174324                 55 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 19 from patent US 6306652.
ACCESSION   AR174324
VERSION     AR174324.1  GI:17914644
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van Der Eb,A.Jan., Bout,A.
            and Valerio,D.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: US 6306652-A 19 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT       12 a      17 c      17 g       9 t
ORIGIN

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Db       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55


RESULT 4
AR183308
LOCUS       AR183308                 55 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 41 from patent US 6340595.
ACCESSION   AR183308
VERSION     AR183308.1  GI:20226901
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Vogels,R., Bout,A., van Es,H. and Schouten,G.
  TITLE     High throughput screening of gene function using adenoviral
            libraries for functional genomics applications
  JOURNAL   Patent: US 6340595-A 41 22-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT       12 a      17 c      17 g       9 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.7e-08;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55


RESULT 5
AX080360
LOCUS       AX080360                 55 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 19 from Patent WO0105945.
ACCESSION   AX080360
VERSION     AX080360.1  GI:13159818
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Hoeben,R.C., Bout,A., Valerio,D., van der Eb,A.J., Schouten,G. and
            Fallaux,F.J.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: WO 0105945-A 19 25-JAN-2001;
            Introgene B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide HP/cla1"
BASE COUNT       12 a      17 c      17 g       9 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.7e-08;
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Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55


RESULT 6
AR091517/c
LOCUS       AR091517                 55 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 20 from patent US 5994128.
ACCESSION   AR091517
VERSION     AR091517.1  GI:10018272
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van der Eb,A.Jan., Bout,A.
            and Valerio,D.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: US 5994128-A 20 30-NOV-1999;
FEATURES             Location/Qualifiers
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BASE COUNT        9 a     17 c     17 g     12 t
ORIGIN

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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 7
AR154397/c
LOCUS       AR154397                 55 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 20 from patent US 6238893.
ACCESSION   AR154397
VERSION     AR154397.1  GI:15122450
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Hoeben,R.Cornelis. and Bout,A.
  TITLE     Method for intracellular DNA amplification
  JOURNAL   Patent: US 6238893-A 20 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT        9 a     17 c     17 g     12 t
ORIGIN

  Query Match             92.7%;  Score 51;  DB 6;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-07;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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RESULT 8
AR174325/c
LOCUS       AR174325                 55 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 20 from patent US 6306652.
ACCESSION   AR174325
VERSION     AR174325.1  GI:17914645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van Der Eb,A.Jan., Bout,A.
            and Valerio,D.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: US 6306652-A 20 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT        9 a     17 c     17 g     12 t
ORIGIN

  Query Match             92.7%;  Score 51;  DB 6;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-07;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
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Db     55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 9
AR183309/c
LOCUS       AR183309                 55 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 42 from patent US 6340595.
ACCESSION   AR183309
VERSION     AR183309.1  GI:20226902
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Vogels,R., Bout,A., van Es,H. and Schouten,G.
  TITLE     High throughput screening of gene function using adenoviral
            libraries for functional genomics applications
  JOURNAL   Patent: US 6340595-A 42 22-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT        9 a     17 c     17 g     12 t
ORIGIN

  Query Match             92.7%;  Score 51;  DB 6;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-07;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 10
AX080361/c
LOCUS       AX080361                 55 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 20 from Patent WO0105945.
ACCESSION   AX080361
VERSION     AX080361.1  GI:13159819
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Hoeben,R.C., Bout,A., Valerio,D., van der Eb,A.J., Schouten,G. and
            Fallaux,F.J.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: WO 0105945-A 20 25-JAN-2001;
            Introgene B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide HP/cla2"
BASE COUNT        9 a     17 c     17 g     12 t
ORIGIN

  Query Match             92.7%;  Score 51;  DB 6;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-07;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     55 ATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 5


RESULT 11
AR091514
LOCUS       AR091514                  50 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 17 from patent US 5994128.
ACCESSION   AR091514
VERSION     AR091514.1  GI:10018269
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van der Eb,A.Jan., Bout,A.
            and Valerio,D.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: US 5994128-A 17 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       10 a     17 c     17 g      6 t
ORIGIN

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  Best Local Similarity   98.0%;  Pred. No. 1e-05;
  Matches   48;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49
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Db      1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49


RESULT 12
AR154394
LOCUS       AR154394                  50 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 17 from patent US 6238893.
ACCESSION   AR154394
VERSION     AR154394.1  GI:15122447
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Hoeben,R.Cornelis. and Bout,A.
  TITLE     Method for intracellular DNA amplification
  JOURNAL   Patent: US 6238893-A 17 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       10 a     17 c     17 g      6 t
ORIGIN

  Query Match             86.2%;  Score 47.4;  DB 6;  Length 50;
  Best Local Similarity   98.0%;  Pred. No. 1e-05;
  Matches   48;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49
          ||||| |||||||||||||||||||||||||||||||||||||||||||
Db      1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49


RESULT 13
AR174322
LOCUS       AR174322                  50 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 17 from patent US 6306652.
ACCESSION   AR174322
VERSION     AR174322.1  GI:17914642
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van Der Eb,A.Jan., Bout,A.
            and Valerio,D.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: US 6306652-A 17 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       10 a     17 c     17 g      6 t
ORIGIN

  Query Match             86.2%;  Score 47.4;  DB 6;  Length 50;
  Best Local Similarity   98.0%;  Pred. No. 1e-05;
  Matches   48;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49
          ||||| |||||||||||||||||||||||||||||||||||||||||||
Db      1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49


RESULT 14
AR183306
LOCUS       AR183306                  50 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 39 from patent US 6340595.
ACCESSION   AR183306
VERSION     AR183306.1  GI:20226899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Vogels,R., Bout,A., van Es,H. and Schouten,G.
  TITLE     High throughput screening of gene function using adenoviral
            libraries for functional genomics applications
  JOURNAL   Patent: US 6340595-A 39 22-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       10 a     17 c     17 g      6 t
ORIGIN

  Query Match             86.2%;  Score 47.4;  DB 6;  Length 50;
  Best Local Similarity   98.0%;  Pred. No. 1e-05;
  Matches   48;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49
          ||||| |||||||||||||||||||||||||||||||||||||||||||
Db      1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49


RESULT 15
AX080358
LOCUS       AX080358                  50 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 17 from Patent WO0105945.
ACCESSION   AX080358
VERSION     AX080358.1  GI:13159816
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Hoeben,R.C., Bout,A., Valerio,D., van der Eb,A.J., Schouten,G. and
            Fallaux,F.J.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: WO 0105945-A 17 25-JAN-2001;
            Introgene B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide HP/asp1"
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BASE COUNT       10 a     17 c     17 g      6 t
ORIGIN

  Query Match            86.2%;  Score 47.4;  DB 6;  Length 50;
  Best Local Similarity  98.0%;  Pred. No. 1e-05;
  Matches   48;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49
          ||||| |||||||||||||||||||||||||||||||||||||||||||
Db      1 GTACACTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49


Search completed: December 27, 2002, 05:31:02
Job time : 1333.5 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 04:38:01 ; Search time 1321.5 Seconds
(without alignments)
674.046 Million cell updates/sec

Title: US-09-918-029-19
Perfect score: 55
Sequence: 1 gtacattgacctagtgccgc.....gcggcactaggtcaatcgat 55

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	25.2	45.8	794	10	BE294341	BE294341 601172854
c	2	24.8	45.1	756	10	BE254363	BE254363 601109113
c	3	24.6	44.7	749	12	BG844791	BG844791 1024007G1
c	4	24	43.6	885	9	AL564683	AL564683 AL564683
c	5	23.8	43.3	174	17	AQ588337	AQ588337 CITBI-E1-
	6	23.8	43.3	885	9	AL564683	AL564683 AL564683
c	7	23.6	42.9	1115	13	BM546853	BM546853 AGENCOURT
c	8	23.6	42.9	1208	12	BG474535	BG474535 602517304
	9	23.4	42.5	596	12	BG194272	BG194272 RST13417
	10	23.4	42.5	884	14	BQ892955	BQ892955 AGENCOURT
	11	23.4	42.5	1149	14	BQ642928	BQ642928 AGENCOURT
	12	23.2	42.2	344	9	AA081549	AA081549 zn21g07.r
c	13	23.2	42.2	590	17	AZ205863	AZ205863 SP_0105_A
	14	23.2	42.2	633	13	BI548352	BI548352 603189633
	15	23.2	42.2	682	13	BI669165	BI669165 603295596
	16	23.2	42.2	703	10	BE381912	BE381912 601272452
	17	23.2	42.2	749	12	BG722376	BG722376 602693574
	18	23.2	42.2	755	12	BG719715	BG719715 602690436
	19	23.2	42.2	814	12	BG717933	BG717933 602693988
	20	23.2	42.2	816	13	BI464399	BI464399 603204058
	21	23.2	42.2	901	12	BG470218	BG470218 602533732
	22	23.2	42.2	1049	14	BQ068336	BQ068336 AGENCOURT
	23	23.2	42.2	1135	12	BG536831	BG536831 602566369
	24	23.2	42.2	1235	14	BQ225342	BQ225342 AGENCOURT
c	25	23	41.8	530	13	BI727969	BI727969 1031095H0
c	26	23	41.8	597	14	BQ818268	BQ818268 1030069F1
c	27	23	41.8	607	13	BI726556	BI726556 1031086A0
c	28	23	41.8	670	14	BQ819135	BQ819135 1030075G0
c	29	23	41.8	708	14	BQ813738	BQ813738 1030038F0
c	30	23	41.8	714	12	BG848999	BG848999 1024023E1
c	31	23	41.8	720	12	BG849000	BG849000 1024023E1
c	32	23	41.8	820	13	BG923596	BG923596 602823455
c	33	23	41.8	822	17	CNS021IX	AL176946 Tetraodon
c	34	23	41.8	906	17	CNS03A5J	AL234784 Tetraodon
c	35	23	41.8	977	14	BQ672537	BQ672537 AGENCOURT
c	36	23	41.8	1030	14	BQ051246	BQ051246 AGENCOURT
c	37	22.8	41.5	319	17	AQ357767	AQ357767 CITBI-E1-
c	38	22.8	41.5	344	9	AA081549	AA081549 zn21g07.r
c	39	22.8	41.5	526	14	BQ812739	BQ812739 1030032A0
c	40	22.8	41.5	565	12	BE725257	BE725257 894082A06
	41	22.8	41.5	592	9	AL703582	AL703582 DKFZp686C
	42	22.8	41.5	599	17	AQ995699	AQ995699 RPCI-23-3
c	43	22.8	41.5	658	12	BG724427	BG724427 602693726
c	44	22.8	41.5	749	12	BG722376	BG722376 602693574
c	45	22.8	41.5	755	12	BG719715	BG719715 602690436

ALIGNMENTS

RESULT 1
BE294341
LOCUS BE294341 794 bp mRNA linear EST 20-JUL-2000
DEFINITION 601172854F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528349 5', mRNA sequence.
ACCESSION BE294341
VERSION BE294341.1 GI:9177788
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 794)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM197 row: 1 column: 14
High quality sequence stop: 605.
FEATURES Location/Qualifiers
source 1. .794
/organism="Homo sapiens"

```
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3528349"
                     /clone_lib="NIH_MGC_17"
                     /tissue_type="rhabdomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      193 a    226 c    216 g    159 t
ORIGIN

  Query Match             45.8%;  Score 25.2;  DB 10;  Length 794;
  Best Local Similarity   66.7%;  Pred. No. 1.8e+02;
  Matches   36;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGA 54
           | |||    || | || | |||||| | | |||| | |||||||||| | |  ||
Db     631 GCACAAGACCCCAATGGCCCCCGGGAACATCCCGAGGGGCACTAGGCCCAGGGA 684


RESULT 2
BE254363/c
LOCUS       BE254363                 756 bp    mRNA    linear   EST 13-JUL-2000
DEFINITION  601109113F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350090 5',
            mRNA sequence.
ACCESSION   BE254363
VERSION     BE254363.1  GI:9124791
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM145  row: i  column: 03
            High quality sequence stop: 668.
FEATURES             Location/Qualifiers
     source          1. .756
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3350090"
                     /clone_lib="NIH_MGC_16"
                     /tissue_type="retinoblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      115 a    197 c    275 g    169 t
ORIGIN

  Query Match             45.1%;  Score 24.8;  DB 10;  Length 756;
  Best Local Similarity   72.7%;  Pred. No. 2.4e+02;
  Matches   32;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy       9 ACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATC 52
             ||| || |||  ||||||| ||||  || |||| ||| || ||
Db     228 ACCCAGGGCCCGCCGGGCACCGCCCCAGCTGCACCAGGCCAGTC 185


RESULT 3
BG844791/c
LOCUS       BG844791                 749 bp    mRNA    linear   EST 29-MAY-2001
DEFINITION  1024007G11.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II
            Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION   BG844791
VERSION     BG844791.1  GI:14225975
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii.
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 749)
  AUTHORS   Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
            McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants; project phase 2
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Charles Hauser
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000
            Tel: 919 613 8159
            Fax: 919 613 8177
            Email: chauser@duke.edu.
FEATURES             Location/Qualifiers
     source          1. .749
                     /organism="Chlamydomonas reinhardtii"
                     /strain="CC-1690 wild type mt+ 21gr"
                     /db_xref="taxon:3055"
                     /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                     II"
                     /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                     XhoI; This library, constructed by John Davies and Jeffrey
                     McDermott, combines cDNAs from CC-1690 cells grown to
                     mid-log phase in TAP (acetate-containing) medium in the
                     light, TAP medium in the dark, HS (minimal) medium in
                     ambient levels of CO2 and HS medium bubbled with 5% CO2.
                     PolyA mRNA was purified from each sample, pooled and cDNA
                     synthesized. The cDNA was directionally cloned into lambda
                     ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
                     pBluescript II SK- plasmids were excised from the lambda
                     ZAP clones by superinfection with ExAssist (Stratagene)
                     phage. The library was normalized using method 4 described
                     in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT      198 a    236 c    155 g    160 t
ORIGIN

  Query Match             44.7%;  Score 24.6;  DB 12;  Length 749;
  Best Local Similarity   65.5%;  Pred. No. 2.8e+02;
  Matches   36;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
           |||  ||  || ||| |||||| ||| | |   | | |||||| || |||  | |
Db     205 GTATCTTTGCCCAGTACCGCCCCGGCCATGGTTGTGAGGCACTGGGGCAAGTGGT 151


RESULT 4
AL564683/c
LOCUS       AL564683                 885 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL564683 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM007YK12 3
            prime, mRNA sequence.
ACCESSION   AL564683
VERSION     AL564683.1  GI:12915335
KEYWORDS    EST.
SOURCE      human.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 885)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .885
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DM007YK12"
                     /clone_lib="LTI_NFL001_NBC4"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      166 a    253 c    263 g    159 t     44 others
ORIGIN

  Query Match             43.6%;  Score 24;  DB 9;  Length 885;
  Best Local Similarity   63.5%;  Pred. No. 4.7e+02;
  Matches   33;  Conservative    2;  Mismatches   17;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATC 52
           | |  | |: | :||| ||| || ||  ||| |  |||||||| | |||| |
Db     612 GMAGGTGGMGCSMGTGTCGCGCGAGCTCAGCACCTGCGGCACTTGTTCAAGC 561


RESULT 5
AQ588337/c
LOCUS       AQ588337                 174 bp    DNA     linear   GSS 07-JUN-1999
DEFINITION  CITBI-E1-2644P17.TR CITBI-E1 Homo sapiens genomic clone 2644P17,
            DNA sequence.
ACCESSION   AQ588337
VERSION     AQ588337.1  GI:5015017
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 174)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2644P17.TF
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .174
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="2644P17"
                     /clone_lib="CITBI-E1"
                     /sex="male"
                     /cell_type="sperm"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
BASE COUNT       47 a     47 c     49 g     30 t      1 others
ORIGIN

  Query Match             43.3%;  Score 23.8;  DB 17;  Length 174;
  Best Local Similarity   72.1%;  Pred. No. 3.6e+02;
  Matches   31;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy       8 GACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAA 50
           |||||  |||   ||||| |||||| ||  || |||| | |||
Db     118 GACCTTCTGCTCTCCGGGGAAAGCCAGGTAGGTACTAAGGCAA 76


RESULT 6
AL564683
LOCUS       AL564683                 885 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL564683 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM007YK12 3
            prime, mRNA sequence.
ACCESSION   AL564683
VERSION     AL564683.1  GI:12915335
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 885)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .885
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DM007YK12"
                     /clone_lib="LTI_NFL001_NBC4"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      166 a    253 c    263 g    159 t     44 others
ORIGIN

  Query Match             43.3%;  Score 23.8;  DB 9;  Length 885;
  Best Local Similarity   66.0%;  Pred. No. 5.5e+02;
  Matches   31;  Conservative    2;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       6 TTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATC 52
           |||| | ||||||||  | ||  ||| || ||| |||: | :| | |
Db     563 TTGAACAAGTGCCGCAGGTGCTGAGCTCGCGCGACACKSGCKCCACC 609
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RESULT 7
BM546853/c
LOCUS       BM546853                1115 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6491290 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723591
            5', mRNA sequence.
ACCESSION   BM546853
VERSION     BM546853.1  GI:18780144
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1115)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12711  row: h  column: 24
            High quality sequence start: 102
            High quality sequence stop: 420.
FEATURES             Location/Qualifiers
     source          1. .1115
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5723591"
                     /clone_lib="NIH_MGC_125"
                     /lab_host="DH10B"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.1 kb, insert size range 1-3.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 036."
BASE COUNT      196 a    365 c    343 g    208 t      3 others
ORIGIN

  Query Match             42.9%;  Score 23.6;  DB 13;  Length 1115;
  Best Local Similarity   69.6%;  Pred. No. 6.8e+02;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       4 CATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCA 49
           |||  ||| || ||||||| |||||  || || |  | || | |||
Db      52 CATCCACCGAGAGCCGCCCAGGCAATCCCAGGTCCCCGCTCGCTCA 7


RESULT 8
BG474535/c
LOCUS       BG474535                1208 bp    mRNA    linear   EST 21-MAR-2001
DEFINITION  602517304F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4649112 5',
            mRNA sequence.
ACCESSION   BG474535
VERSION     BG474535.1  GI:13406812
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1208)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM1428  row: g  column: 01
            High quality sequence stop: 478.
FEATURES             Location/Qualifiers
     source          1. .1208
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4649112"
                     /clone_lib="NIH_MGC_16"
                     /tissue_type="retinoblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      361 a    349 c    313 g    185 t
ORIGIN

  Query Match             42.9%;  Score 23.6;  DB 12;  Length 1208;
  Best Local Similarity   69.6%;  Pred. No. 7e+02;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGG 46
           |||||||| ||| || || | ||| |  ||| || | | |||  ||
Db    1008 GTACATTGCCCTTGTTCCCCGCGGTCTCAGCACGCGTGTCACGTGG 963


RESULT 9
BG194272
LOCUS       BG194272                596 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST13417 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG194272
VERSION     BG194272.1  GI:13715959
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 596)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 596.
FEATURES             Location/Qualifiers
     source          1. .596
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
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Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT 181 a 140 c 126 g 148 t 1 others
ORIGIN

Query Match 42.5%; Score 23.4; DB 12; Length 596;
Best Local Similarity 67.3%; Pred. No. 6.8e+02;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 4 CATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATC 52
Db 6 CCTTGACCAGGTCTAGCCTTGGCAGAGCAAGGGAGCCACTAAGCCAAAC 54

RESULT 10
BQ892955
LOCUS BQ892955 884 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT_8124301 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6178096 5', mRNA sequence.
ACCESSION BQ892955
VERSION BQ892955.1 GI:22284969
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 884)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI3557 row: b column: 17
High quality sequence stop: 629.
FEATURES Location/Qualifiers
source 1. .884
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6178096"
/clone_lib="Lupski_dorsal_root_ganglion"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."
BASE COUNT 226 a 215 c 335 g 108 t
ORIGIN

Query Match 42.5%; Score 23.4; DB 14; Length 884;
Best Local Similarity 73.2%; Pred. No. 7.5e+02;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GTACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCA 41
Db 826 GGACATGGCCCTGGACCCCCCCGGCCCAATCCCGGGGGGCA 866

RESULT 11
BQ642928
LOCUS BQ642928 1149 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT_8485188 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:6305160 5', mRNA sequence.
ACCESSION BQ642928
VERSION BQ642928.1 GI:21767100
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1149)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2527 row: a column: 01
High quality sequence start: 53
High quality sequence stop: 327.
FEATURES Location/Qualifiers
source 1. .1149
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6305160"
/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 162 a 442 c 398 g 140 t 7 others
ORIGIN

Query Match 42.5%; Score 23.4; DB 14; Length 1149;
Best Local Similarity 73.2%; Pred. No. 8e+02;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 3 ACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACT 43
Db 453 ACTTTGGGCGAGTGCCGCCCGCGGCACGCGCGGGCGCCCCT 493

RESULT 12
AA081549
LOCUS AA081549 344 bp mRNA linear EST 21-OCT-1996
DEFINITION zn21g07.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548124 5', mRNA sequence.
ACCESSION AA081549
VERSION AA081549.1 GI:1623779
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 344)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

```
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 326.
FEATURES             Location/Qualifiers
     source          1. .344
                     /organism="Homo sapiens"
                     /db_xref="GDB:3926640"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:548124"
                     /clone_lib="Stratagene neuroepithelium NT2RAMI 937234"
                     /dev_stage="Ntera-2/RA+MI neuroepithelial cells"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Cloned unidirectionally.  Primer: Oligo dT. NT2
                     (Ntera-2/c1.D1)  precursor cells induced with Retinoic
                     Acid for 1 week, followed by 3 weeks in mitotic inhibitors
                     (Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR
                     Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3'
                     adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT       85 a    102 c     84 g     71 t      2 others
ORIGIN

  Query Match             42.2%;  Score 23.2;  DB 9;  Length 344;
  Best Local Similarity   70.5%;  Pred. No. 6.9e+02;
  Matches   31;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       3 ACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGG 46
          ||| | ||| || |||| |  ||   |||| |||||| |||||
Db      41 ACAGTTACCCAGCGCCGGACTCGCTGCGCCCCGGCGGCTCTAGG 84


RESULT 13
AZ205863/c
LOCUS       AZ205863                590 bp    DNA     linear   GSS 31-AUG-2000
DEFINITION  SP_0105_A1_F05_T7A Strongylocentrotus purpuratus, purple sea urchin
            , sperm genomic BAC library Strongylocentrotus purpuratus genomic
            clone Plate=105 Col=9 Row=K, DNA sequence.
ACCESSION   AZ205863
VERSION     AZ205863.1  GI:8415870
KEYWORDS    GSS.
SOURCE      Strongylocentrotus purpuratus.
  ORGANISM  Strongylocentrotus purpuratus
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoida;
            Strongylocentrotidae; Strongylocentrotus.
REFERENCE   1  (bases 1 to 590)
  AUTHORS   Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
            Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray
            ,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. and
            Hood,L.
  TITLE     A sea urchin genome project: Sequence scan, virtual map, and
            additional resources
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
  MEDLINE   20402566
COMMENT     Contact: Cameron, RA, Davidson, EH, Hood, L
            Division of Biology 156-29
            California Institute of Technology
            Pasadena California 91125, USA
            Tel: (626) 395-8421
            Fax: (626) 793-3047
            Email: acameron@caltech.edu
            Plate: 105  row: K  column: 9
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 590.
FEATURES             Location/Qualifiers
     source          1. .590
                     /organism="Strongylocentrotus purpuratus"
                     /db_xref="taxon:7668"
                     /clone="Plate=105 Col=9 Row=K"
                     /clone_lib="Strongylocentrotus purpuratus, purple sea
                     urchin, sperm genomic BAC library"
                     /note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                     DH10B"
BASE COUNT      163 a    157 c    110 g    159 t      1 others
ORIGIN

  Query Match             42.2%;  Score 23.2;  DB 17;  Length 590;
  Best Local Similarity   65.4%;  Pred. No. 7.9e+02;
  Matches   34;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy       4 CATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGGTCAATCGAT 55
           |||| |  ||||||  | || |||  || | | | |||||  || | | |||
Db     218 CATTCAGTTAGTGCGACACGTGCATCGCTCTGTCAGCACTGTGTGAGTTGAT 167


RESULT 14
BI548352
LOCUS       BI548352                633 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603189633F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5260712 5',
            mRNA sequence.
ACCESSION   BI548352
VERSION     BI548352.1  GI:15435664
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11657  row: b  column: 09
            High quality sequence stop: 630.
FEATURES             Location/Qualifiers
     source          1. .633
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5260712"
                     /clone_lib="NIH_MGC_95"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for  full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health).  Note: this is a NIH_MGC Library."
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BASE COUNT      133 a    193 c    148 g    159 t
ORIGIN

  Query Match             42.2%;  Score 23.2;  DB 13;  Length 633;
  Best Local Similarity   70.5%;  Pred. No. 8e+02;
  Matches   31;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       3 ACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGG 46
           ||| |  || || ||||  || ||   |||| |||||| |||||
Db      30 ACAGTCCCCCAGCGCCGGACGCGCCGCGCCCTGGCGGCTCTAGG 73


RESULT 15
BI669165
LOCUS       BI669165                682 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603295596F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5314822 5',
            mRNA sequence.
ACCESSION   BI669165
VERSION     BI669165.1  GI:15583398
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 682)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11797  row: p  column: 23
            High quality sequence stop: 682.
FEATURES             Location/Qualifiers
     source          1. .682
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5314822"
                     /clone_lib="NIH_MGC_96"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.3 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length  clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      159 a    176 c    184 g    163 t
ORIGIN

  Query Match             42.2%;  Score 23.2;  DB 13;  Length 682;
  Best Local Similarity   70.5%;  Pred. No. 8.2e+02;
  Matches   31;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       3 ACATTGACCTAGTGCCGCCCGGGCAAAGCCCGGGCGGCACTAGG 46
           ||| |  || || ||||  || ||   |||| |||||| |||||
Db      73 ACAGTCCCCCAGCGCCGGACGCGCCGCGCCCTGGCGGCTCTAGG 116


Search completed: December 27, 2002, 06:15:34
Job time : 1327.5 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 03:13:39 ; Search time 1330 Seconds
(without alignments)
1203.499 Million cell updates/sec

Title: US-09-918-029-20
Perfect score: 55
Sequence: 1 gtacatcgattgacctagtg.....ccgggcggcactaggtcaat 55

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	55	6	AR091517	AR091517 Sequence
2	55	100.0	55	6	AR154397	AR154397 Sequence
3	55	100.0	55	6	AR174325	AR174325 Sequence
4	55	100.0	55	6	AR183309	AR183309 Sequence
5	55	100.0	55	6	AX080361	AX080361 Sequence
c 6	51	92.7	55	6	AR091516	AR091516 Sequence
c 7	51	92.7	55	6	AR154396	AR154396 Sequence
c 8	51	92.7	55	6	AR174324	AR174324 Sequence
c 9	51	92.7	55	6	AR183308	AR183308 Sequence
c 10	51	92.7	55	6	AX080360	AX080360 Sequence
c 11	43.4	78.9	50	6	AR091514	AR091514 Sequence
12	43.4	78.9	50	6	AR091515	AR091515 Sequence
c 13	43.4	78.9	50	6	AR154394	AR154394 Sequence
14	43.4	78.9	50	6	AR154395	AR154395 Sequence
c 15	43.4	78.9	50	6	AR174322	AR174322 Sequence
16	43.4	78.9	50	6	AR174323	AR174323 Sequence
c 17	43.4	78.9	50	6	AR183306	AR183306 Sequence
18	43.4	78.9	50	6	AR183307	AR183307 Sequence
c 19	43.4	78.9	50	6	AX080358	AX080358 Sequence
20	43.4	78.9	50	6	AX080359	AX080359 Sequence
21	42.2	76.7	55	6	AR091516	AR091516 Sequence
c 22	42.2	76.7	55	6	AR091517	AR091517 Sequence
23	42.2	76.7	55	6	AR154396	AR154396 Sequence
c 24	42.2	76.7	55	6	AR154397	AR154397 Sequence
25	42.2	76.7	55	6	AR174324	AR174324 Sequence
c 26	42.2	76.7	55	6	AR174325	AR174325 Sequence
27	42.2	76.7	55	6	AR183308	AR183308 Sequence
c 28	42.2	76.7	55	6	AR183309	AR183309 Sequence
29	42.2	76.7	55	6	AX080360	AX080360 Sequence
c 30	42.2	76.7	55	6	AX080361	AX080361 Sequence
c 31	39.4	71.6	45	6	AR091519	AR091519 Sequence
c 32	39.4	71.6	45	6	AR154399	AR154399 Sequence
c 33	39.4	71.6	45	6	AR174327	AR174327 Sequence
c 34	39.4	71.6	45	6	AR183314	AR183314 Sequence
35	38.6	70.2	50	6	AR091514	AR091514 Sequence
c 36	38.6	70.2	50	6	AR091515	AR091515 Sequence
37	38.6	70.2	50	6	AR154394	AR154394 Sequence
c 38	38.6	70.2	50	6	AR154395	AR154395 Sequence
39	38.6	70.2	50	6	AR174322	AR174322 Sequence
c 40	38.6	70.2	50	6	AR174323	AR174323 Sequence
41	38.6	70.2	50	6	AR183306	AR183306 Sequence
c 42	38.6	70.2	50	6	AR183307	AR183307 Sequence
43	38.6	70.2	50	6	AX080358	AX080358 Sequence
c 44	38.6	70.2	50	6	AX080359	AX080359 Sequence
c 45	36.2	65.8	45	6	AX080363	AX080363 Sequence

ALIGNMENTS

RESULT 1
AR091517
LOCUS AR091517 55 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 20 from patent US 5994128.
ACCESSION AR091517
VERSION AR091517.1 GI:10018272
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 55)
AUTHORS Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van der Eb,A.Jan., Bout,A. and Valerio,D.
TITLE Packaging systems for human recombinant adenovirus to be used in gene therapy

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  JOURNAL   Patent: US 5994128-A 20 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT        9 a     17 c     17 g     12 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 2.4e-08;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 2
AR154397
LOCUS       AR154397                 55 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 20 from patent US 6238893.
ACCESSION   AR154397
VERSION     AR154397.1  GI:15122450
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Hoeben,R.Cornelis. and Bout,A.
  TITLE     Method for intracellular DNA amplification
  JOURNAL   Patent: US 6238893-A 20 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT        9 a     17 c     17 g     12 t
ORIGIN

  Query Match           100.0%;  Score 55;  DB 6;  Length 55;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-08;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 3
AR174325
LOCUS       AR174325                 55 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 20 from patent US 6306652.
ACCESSION   AR174325
VERSION     AR174325.1  GI:17914645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van Der Eb,A.Jan., Bout,A.
            and Valerio,D.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: US 6306652-A 20 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT        9 a     17 c     17 g     12 t
ORIGIN

  Query Match           100.0%;  Score 55;  DB 6;  Length 55;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-08;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 4
AR183309
LOCUS       AR183309                 55 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 42 from patent US 6340595.
ACCESSION   AR183309
VERSION     AR183309.1  GI:20226902
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Vogels,R., Bout,A., van Es,H. and Schouten,G.
  TITLE     High throughput screening of gene function using adenoviral
            libraries for functional genomics applications
  JOURNAL   Patent: US 6340595-A 42 22-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT        9 a     17 c     17 g     12 t
ORIGIN

  Query Match           100.0%;  Score 55;  DB 6;  Length 55;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-08;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 5
AX080361
LOCUS       AX080361                 55 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 20 from Patent WO0105945.
ACCESSION   AX080361
VERSION     AX080361.1  GI:13159819
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Hoeben,R.C., Bout,A., Valerio,D., van der Eb,A.J., Schouten,G. and
            Fallaux,F.J.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: WO 0105945-A 20 25-JAN-2001;
            Introgene B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide HP/cla2"
BASE COUNT        9 a     17 c     17 g     12 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 2.4e-08;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 6
AR091516/c
LOCUS       AR091516                 55 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 19 from patent US 5994128.
ACCESSION   AR091516
VERSION     AR091516.1  GI:10018271
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van der Eb,A.Jan., Bout,A.
            and Valerio,D.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: US 5994128-A 19 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT       12 a     17 c     17 g      9 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.5e-07;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 7
AR154396/c
LOCUS       AR154396                 55 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 19 from patent US 6238893.
ACCESSION   AR154396
VERSION     AR154396.1  GI:15122449
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Hoeben,R.Cornelis. and Bout,A.
  TITLE     Method for intracellular DNA amplification
  JOURNAL   Patent: US 6238893-A 19 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT       12 a     17 c     17 g      9 t
ORIGIN

  Query Match             92.7%;  Score 51;  DB 6;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-07;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db     55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 8
AR174324/c
LOCUS       AR174324                 55 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 19 from patent US 6306652.
ACCESSION   AR174324
VERSION     AR174324.1  GI:17914644
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van Der Eb,A.Jan., Bout,A.
            and Valerio,D.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: US 6306652-A 19 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT       12 a     17 c     17 g      9 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.5e-07;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db     55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 9
AR183308/c
LOCUS       AR183308                 55 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 41 from patent US 6340595.
ACCESSION   AR183308
VERSION     AR183308.1  GI:20226901
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Vogels,R., Bout,A., van Es,H. and Schouten,G.
  TITLE     High throughput screening of gene function using adenoviral
            libraries for functional genomics applications
  JOURNAL   Patent: US 6340595-A 41 22-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="unknown"
BASE COUNT       12 a     17 c     17 g      9 t
ORIGIN

  Query Match             92.7%;  Score 51;  DB 6;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-07;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 10
AX080360/c
LOCUS       AX080360                 55 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 19 from Patent WO0105945.
ACCESSION   AX080360
VERSION     AX080360.1  GI:13159818
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Hoeben,R.C., Bout,A., Valerio,D., van der Eb,A.J., Schouten,G. and
            Fallaux,F.J.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: WO 0105945-A 19 25-JAN-2001;
            Introgene B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide HP/cla1"
BASE COUNT       12 a     17 c     17 g      9 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.5e-07;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 11
AR091514/c
LOCUS       AR091514                  50 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 17 from patent US 5994128.
ACCESSION   AR091514
VERSION     AR091514.1  GI:10018269
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van der Eb,A.Jan., Bout,A.
            and Valerio,D.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: US 5994128-A 17 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       10 a     17 c     17 g      6 t
ORIGIN

  Query Match             78.9%;  Score 43.4;  DB 6;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 0.00021;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db      49 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 5


RESULT 12
AR091515
LOCUS       AR091515                  50 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 18 from patent US 5994128.
ACCESSION   AR091515
VERSION     AR091515.1  GI:10018270
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van der Eb,A.Jan., Bout,A.
            and Valerio,D.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: US 5994128-A 18 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT        6 a     17 c     17 g     10 t
ORIGIN

  Query Match             78.9%;  Score 43.4;  DB 6;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 0.00021;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           ||||||||||||||||||||||||||||||||||||||||||||| |
Db       6 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 50


RESULT 13
AR154394/c
LOCUS       AR154394                  50 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 17 from patent US 6238893.
ACCESSION   AR154394
VERSION     AR154394.1  GI:15122447
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Hoeben,R.Cornelis. and Bout,A.
  TITLE     Method for intracellular DNA amplification
  JOURNAL   Patent: US 6238893-A 17 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       10 a     17 c     17 g      6 t
ORIGIN

  Query Match             78.9%;  Score 43.4;  DB 6;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 0.00021;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           ||||||||||||||||||||||||||||||||||||||||||||| |
Db      49 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 5


RESULT 14
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LOCUS       AR154395                  50 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 18 from patent US 6238893.
ACCESSION   AR154395
VERSION     AR154395.1  GI:15122448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Hoeben,R.Cornelis. and Bout,A.
  TITLE     Method for intracellular DNA amplification
  JOURNAL   Patent: US 6238893-A 18 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT        6 a     17 c     17 g     10 t
ORIGIN

  Query Match             78.9%;  Score 43.4;  DB 6;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 0.00021;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db       6 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 50


RESULT 15
AR174322/c
LOCUS       AR174322                  50 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 17 from patent US 6306652.
ACCESSION   AR174322
VERSION     AR174322.1  GI:17914642
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Fallaux,F.Jacobus., Hoeben,R.Cornelis., Van Der Eb,A.Jan., Bout,A.
            and Valerio,D.
  TITLE     Packaging systems for human recombinant adenovirus to be used in
            gene therapy
  JOURNAL   Patent: US 6306652-A 17 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       10 a     17 c     17 g      6 t
ORIGIN

  Query Match             78.9%;  Score 43.4;  DB 6;  Length 50;
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Best Local Similarity 97.8%; Pred. No. 0.00021;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           ||||||||||||||||||||||||||||||||||||||||||| |
Db      49 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 5
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Search completed: December 27, 2002, 05:31:03
Job time : 1332.5 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 04:38:45 ; Search time 33 Seconds
(without alignments)
511.128 Million cell updates/sec

Title: US-09-918-029-20
Perfect score: 55
Sequence: 1 gtacatcgattgacctagtg.....ccgggcggcactaggtcaat 55

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	55	100.0	55	2	US-08-793-170-20	Sequence 20, Appl
	2	55	100.0	55	3	US-08-892-873-20	Sequence 20, Appl
	3	55	100.0	55	4	US-09-334-765A-20	Sequence 20, Appl
	4	55	100.0	55	4	US-09-356-575E-20	Sequence 20, Appl
	5	55	100.0	55	4	US-09-333-820-20	Sequence 20, Appl
	6	55	100.0	55	4	US-09-358-036-42	Sequence 42, Appl
	7	55	100.0	55	4	US-09-097-239-42	Sequence 42, Appl
c	8	51	92.7	55	2	US-08-793-170-19	Sequence 19, Appl
c	9	51	92.7	55	3	US-08-892-873-19	Sequence 19, Appl
c	10	51	92.7	55	4	US-09-334-765A-19	Sequence 19, Appl
c	11	51	92.7	55	4	US-09-356-575E-19	Sequence 19, Appl
c	12	51	92.7	55	4	US-09-333-820-19	Sequence 19, Appl
c	13	51	92.7	55	4	US-09-358-036-41	Sequence 41, Appl
c	14	51	92.7	55	4	US-09-097-239-41	Sequence 41, Appl
c	15	43.4	78.9	50	2	US-08-793-170-17	Sequence 17, Appl
	16	43.4	78.9	50	2	US-08-793-170-18	Sequence 18, Appl
c	17	43.4	78.9	50	3	US-08-892-873-17	Sequence 17, Appl
	18	43.4	78.9	50	3	US-08-892-873-18	Sequence 18, Appl
c	19	43.4	78.9	50	4	US-09-334-765A-17	Sequence 17, Appl
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c	23	43.4	78.9	50	4	US-09-333-820-17	Sequence 17, Appl
	24	43.4	78.9	50	4	US-09-333-820-18	Sequence 18, Appl
c	25	43.4	78.9	50	4	US-09-358-036-39	Sequence 39, Appl
	26	43.4	78.9	50	4	US-09-358-036-40	Sequence 40, Appl
c	27	43.4	78.9	50	4	US-09-097-239-39	Sequence 39, Appl
	28	43.4	78.9	50	4	US-09-097-239-40	Sequence 40, Appl
	29	42.2	76.7	55	2	US-08-793-170-19	Sequence 19, Appl
c	30	42.2	76.7	55	2	US-08-793-170-20	Sequence 20, Appl
	31	42.2	76.7	55	3	US-08-892-873-19	Sequence 19, Appl
c	32	42.2	76.7	55	3	US-08-892-873-20	Sequence 20, Appl
	33	42.2	76.7	55	4	US-09-334-765A-19	Sequence 19, Appl
c	34	42.2	76.7	55	4	US-09-334-765A-20	Sequence 20, Appl
	35	42.2	76.7	55	4	US-09-356-575E-19	Sequence 19, Appl
c	36	42.2	76.7	55	4	US-09-356-575E-20	Sequence 20, Appl
	37	42.2	76.7	55	4	US-09-333-820-19	Sequence 19, Appl
c	38	42.2	76.7	55	4	US-09-333-820-20	Sequence 20, Appl
	39	42.2	76.7	55	4	US-09-358-036-41	Sequence 41, Appl
c	40	42.2	76.7	55	4	US-09-358-036-42	Sequence 42, Appl
	41	42.2	76.7	55	4	US-09-097-239-41	Sequence 41, Appl
c	42	42.2	76.7	55	4	US-09-097-239-42	Sequence 42, Appl
c	43	39.4	71.6	45	2	US-08-793-170-22	Sequence 22, Appl
c	44	39.4	71.6	45	3	US-08-892-873-22	Sequence 22, Appl
c	45	39.4	71.6	45	4	US-09-334-765A-22	Sequence 22, Appl

ALIGNMENTS

```
RESULT 1
US-08-793-170-20
; Sequence 20, Application US/08793170
; Patent No. 5994128
;  GENERAL INFORMATION:
;    APPLICANT:  FALLAUX et al.
;    TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT
;    TITLE OF INVENTION:  ADENOVIRUS TO BE USED IN GENE THERAPY
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
;      STREET:  260 SHERIDAN AVENUE, PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,170
;      FILING DATE:  25-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO 97/00326
;      FILING DATE:  14-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201728.3
;      FILING DATE:  26-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201611.1
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.002.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-3377
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  55 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-793-170-20
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  Best Local Similarity   100.0%;  Pred. No. 5.7e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 2
US-08-892-873-20
; Sequence 20, Application US/08892873
; Patent No. 6033908
;  GENERAL INFORMATION:
;    APPLICANT:  FALLAUX et al.
;    TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT
;    TITLE OF INVENTION:  ADENOVIRUS TO BE USED IN GENE THERAPY
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
;      STREET:  260 SHERIDAN AVENUE, PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/892,873
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/793,170
;      FILING DATE:  25-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO 97/00326
;      FILING DATE:  14-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201728.3
;      FILING DATE:  26-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201611.1
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.002.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-3377
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  55 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-892-873-20

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  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 3
US-09-334-765A-20
; Sequence 20, Application US/09334765A
; Patent No. 6238893
; GENERAL INFORMATION:
;  APPLICANT:  Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO BE USED
;  TITLE OF INVENTION:  IN GENE THERAPY
;  FILE REFERENCE:  3833.2US
;  CURRENT APPLICATION NUMBER: US/09/334,765A
;  CURRENT FILING DATE:  1999-06-16
;  PRIOR APPLICATION NUMBER:  US 08/793,170
;  PRIOR FILING DATE:  1997-03-25
;  PRIOR APPLICATION NUMBER:  PCT/NL96/00244
;  PRIOR FILING DATE:  1996-06-14
;  PRIOR APPLICATION NUMBER:  EP 95201728.3
;  PRIOR FILING DATE:  1995-06-26
;  PRIOR APPLICATION NUMBER:  EP 95201611.1
;  PRIOR FILING DATE:  1995-06-15
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  Corel WordPerfect 8.0
; SEQ ID NO 20
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: primer HP/cla2
US-09-334-765A-20

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  Best Local Similarity   100.0%;  Pred. No. 5.7e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 4
US-09-356-575E-20
; Sequence 20, Application US/09356575E
; Patent No. 6265212
; GENERAL INFORMATION:
;  APPLICANT:  Fallaux, Frits
;  APPLICANT:  Hoeben, Robert
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  van der Eb, Alex
;  APPLICANT:  Schouten, Govert
;  TITLE OF INVENTION:  PACKAGING SYSTEMS
;  FILE REFERENCE:  2578-3935US
;  CURRENT APPLICATION NUMBER: US/09/356,575E
;  CURRENT FILING DATE:  1999-07-19
;  PRIOR APPLICATION NUMBER:  US 08/793,170
;  PRIOR FILING DATE:  1997-03-25
;  PRIOR APPLICATION NUMBER:  PCT/NL96/00244
;  PRIOR FILING DATE:  1996-06-14
;  PRIOR APPLICATION NUMBER:  EP 95201611.1
;  PRIOR FILING DATE:  1995-06-15
;  PRIOR APPLICATION NUMBER:  EP 95201728.3
;  PRIOR FILING DATE:  1995-06-26
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 20
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Unknown
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;   FEATURE:
;   OTHER INFORMATION: Derived from Adenovirus
US-09-356-575E-20

  Query Match            100.0%;  Score 55;  DB 4;  Length 55;
  Best Local Similarity  100.0%;  Pred. No. 5.7e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 5
US-09-333-820-20
; Sequence 20, Application US/09333820A
; Patent No. 6306652
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT: Hoeben, Robert C.
;  APPLICANT: Bout, Abraham
;  APPLICANT: Valerio, Domenico
;  APPLICANT: Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO BE USED IN
;  TITLE OF INVENTION: GENE THERAPY
;  FILE REFERENCE: 3833.1US
;  CURRENT APPLICATION NUMBER: US/09/333,820A
;  CURRENT FILING DATE: 1999-06-15
;  EARLIER APPLICATION NUMBER: US 08/793,170
;  EARLIER FILING DATE: 1997-03-25
;  EARLIER APPLICATION NUMBER: PCT/NL96/00244
;  EARLIER FILING DATE: 1996-06-14
;  EARLIER APPLICATION NUMBER: EP 95201728.3
;  EARLIER FILING DATE: 1995-06-26
;  EARLIER APPLICATION NUMBER: EP 95201611.1
;  EARLIER FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 20
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: primer HP/cla2
US-09-333-820-20

  Query Match            100.0%;  Score 55;  DB 4;  Length 55;
  Best Local Similarity  100.0%;  Pred. No. 5.7e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 6
US-09-358-036-42
; Sequence 42, Application US/09358036
; Patent No. 6340595
; GENERAL INFORMATION:
;  APPLICANT: Vogels, Ronald
;  APPLICANT: Bout, Abraham
;  APPLICANT: van Es, Helmuth
;  APPLICANT: Schouten, Govert
;  TITLE OF INVENTION: High Throughput Screening of Gene Function Using
;  TITLE OF INVENTION: Adenoviral Libraries for Functional Genomics
;  TITLE OF INVENTION: Applications
;  FILE REFERENCE: 21834108
;  CURRENT APPLICATION NUMBER: US/09/358,036
;  CURRENT FILING DATE: 1999-07-21
;  EARLIER APPLICATION NUMBER: US 09/097,239
;  EARLIER FILING DATE: 1995-07-25
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-358-036-42

  Query Match            100.0%;  Score 55;  DB 4;  Length 55;
  Best Local Similarity  100.0%;  Pred. No. 5.7e-11;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 7
US-09-097-239-42
; Sequence 42, Application US/09097239
; Patent No. 6413776
;  GENERAL INFORMATION:
;    APPLICANT:  VOGELS, RONALD,
;    APPLICANT:  BOUT, ABRAHAM,
;    APPLICANT:  VAN ES, HELMUTH HG,
;    APPLICANT:  SCHOUTEN, GOVERT
;    TITLE OF INVENTION:  HIGH THROUGHPUT SCREENING OF GENE
;    TITLE OF INVENTION:  FUNCTION USING ADENOVIRAL LIBRARIES FOR FUNCTIONAL
;    TITLE OF INVENTION:  GENOMICS APPLICATIONS
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/097,239
;      FILING DATE:  12-JUN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.008.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  55 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-09-097-239-42

  Query Match            100.0%;  Score 55;  DB 4;  Length 55;
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  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 8
US-08-793-170-19/c
; Sequence 19, Application US/08793170
; Patent No. 5994128
; GENERAL INFORMATION:
;   APPLICANT:  FALLAUX et al.
;   TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT
;   TITLE OF INVENTION:  ADENOVIRUS TO BE USED IN GENE THERAPY
;   NUMBER OF SEQUENCES:  22
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
;     STREET:  260 SHERIDAN AVENUE, PO BOX 60039
;     CITY:  PALO ALTO
;     STATE:  CALIFORNIA
;     COUNTRY:  USA
;     ZIP:  94306
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/793,170
;     FILING DATE:  25-MAR-1997
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  WO 97/00326
;     FILING DATE:  14-JUN-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  EP 95201728.3
;     FILING DATE:  26-JUN-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  EP 95201611.1
;     FILING DATE:  15-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  RAE-VENTER, BARBARA
;     REGISTRATION NUMBER:  32,750
;     REFERENCE/DOCKET NUMBER:  INGE.002.00US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (650)328-4400
;     TELEFAX:  (650)328-3377
;     TELEX:  N/A
; INFORMATION FOR SEQ ID NO:  19:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  55 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  other nucleic acid
US-08-793-170-19

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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 9
US-08-892-873-19/c
; Sequence 19, Application US/08892873
; Patent No. 6033908
; GENERAL INFORMATION:
;   APPLICANT:  FALLAUX et al.
;   TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT
;   TITLE OF INVENTION:  ADENOVIRUS TO BE USED IN GENE THERAPY
;   NUMBER OF SEQUENCES:  22
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
;     STREET:  260 SHERIDAN AVENUE, PO BOX 60039
;     CITY:  PALO ALTO
;     STATE:  CALIFORNIA
;     COUNTRY:  USA
;     ZIP:  94306
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/892,873
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/793,170
;     FILING DATE:  25-MAR-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  WO 97/00326
;     FILING DATE:  14-JUN-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  EP 95201728.3
;     FILING DATE:  26-JUN-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  EP 95201611.1
;     FILING DATE:  15-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  RAE-VENTER, BARBARA
;     REGISTRATION NUMBER:  32,750
;     REFERENCE/DOCKET NUMBER:  INGE.002.00US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (650)328-4400
;     TELEFAX:  (650)328-3377
;     TELEX:  N/A
; INFORMATION FOR SEQ ID NO:  19:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  55 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  other nucleic acid
US-08-892-873-19

  Query Match             92.7%;  Score 51;  DB 3;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 10
US-09-334-765A-19/c
; Sequence 19, Application US/09334765A
; Patent No. 6238893
; GENERAL INFORMATION:
;  APPLICANT:  Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO BE USED
;  TITLE OF INVENTION:  IN GENE THERAPY
;  FILE REFERENCE:  3833.2US
;  CURRENT APPLICATION NUMBER: US/09/334,765A
;  CURRENT FILING DATE:  1999-06-16
;  PRIOR APPLICATION NUMBER:  US 08/793,170
;  PRIOR FILING DATE:  1997-03-25
;  PRIOR APPLICATION NUMBER:  PCT/NL96/00244
;  PRIOR FILING DATE:  1996-06-14
;  PRIOR APPLICATION NUMBER:  EP 95201728.3
;  PRIOR FILING DATE:  1995-06-26
;  PRIOR APPLICATION NUMBER:  EP 95201611.1
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;  PRIOR FILING DATE:  1995-06-15
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  Corel WordPerfect 8.0
; SEQ ID NO 19
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: PCT primer HP/clal
US-09-334-765A-19

  Query Match             92.7%;  Score 51;  DB 4;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 11
US-09-356-575E-19/c
; Sequence 19, Application US/09356575E
; Patent No. 6265212
; GENERAL INFORMATION:
;  APPLICANT:  Fallaux, Frits
;  APPLICANT:  Hoeben, Robert
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  van der Eb, Alex
;  APPLICANT:  Schouten, Govert
;  TITLE OF INVENTION:  PACKAGING SYSTEMS
;  FILE REFERENCE:  2578-3935US
;  CURRENT APPLICATION NUMBER: US/09/356,575E
;  CURRENT FILING DATE:  1999-07-19
;  PRIOR APPLICATION NUMBER:  US 08/793,170
;  PRIOR FILING DATE:  1997-03-25
;  PRIOR APPLICATION NUMBER:  PCT/NL96/00244
;  PRIOR FILING DATE:  1996-06-14
;  PRIOR APPLICATION NUMBER:  EP 95201611.1
;  PRIOR FILING DATE:  1995-06-15
;  PRIOR APPLICATION NUMBER:  EP 95201728.3
;  PRIOR FILING DATE:  1995-06-26
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Derived from Adenovirus
US-09-356-575E-19

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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 12
US-09-333-820-19/c
; Sequence 19, Application US/09333820A
; Patent No. 6306652
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT: Hoeben, Robert C.
;  APPLICANT: Bout, Abraham
;  APPLICANT: Valerio, Domenico
;  APPLICANT: Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO BE USED
;  TITLE OF INVENTION: GENE THERAPY
;  FILE REFERENCE: 3833.1US
;  CURRENT APPLICATION NUMBER: US/09/333,820A
;  CURRENT FILING DATE: 1999-06-15
;  EARLIER APPLICATION NUMBER: US 08/793,170
;  EARLIER FILING DATE: 1997-03-25
;  EARLIER APPLICATION NUMBER: PCT/NL96/00244
;  EARLIER FILING DATE: 1996-06-14
;  EARLIER APPLICATION NUMBER: EP 95201728.3
;  EARLIER FILING DATE: 1995-06-26
;  EARLIER APPLICATION NUMBER: EP 95201611.1
;  EARLIER FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 19
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: PCT primer HP/clal
US-09-333-820-19

  Query Match             92.7%;  Score 51;  DB 4;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 13
US-09-358-036-41/c
; Sequence 41, Application US/09358036
; Patent No. 6340595
; GENERAL INFORMATION:
;  APPLICANT: Vogels, Ronald
;  APPLICANT: Bout, Abraham
;  APPLICANT: van Es, Helmuth
;  APPLICANT: Schouten, Govert
;  TITLE OF INVENTION: High Throughput Screening of Gene Function Using
;  TITLE OF INVENTION: Adenoviral Libraries for Functional Genomics
;  TITLE OF INVENTION: Applications
;  FILE REFERENCE: 21834108
;  CURRENT APPLICATION NUMBER: US/09/358,036
;  CURRENT FILING DATE: 1999-07-21
;  EARLIER APPLICATION NUMBER: US 09/097,239
;  EARLIER FILING DATE: 1995-07-25
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-358-036-41

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  Best Local Similarity   100.0%;  Pred. No. 1.4e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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RESULT 14
US-09-097-239-41/c
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; Sequence 41, Application US/09097239
; Patent No. 6413776
;  GENERAL INFORMATION:
;    APPLICANT:  VOGELS, RONALD,
;    APPLICANT:  BOUT, ABRAHAM,
;    APPLICANT:  VAN ES, HELMUTH HG,
;    APPLICANT:  SCHOUTEN, GOVERT
;    TITLE OF INVENTION:  HIGH THROUGHPUT SCREENING OF GENE
;    TITLE OF INVENTION:  FUNCTION USING ADENOVIRAL LIBRARIES FOR FUNCTIONAL
;    TITLE OF INVENTION:  GENOMICS APPLICATIONS
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/097,239
;      FILING DATE:  12-JUN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.008.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  55 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-09-097-239-41

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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 15
US-08-793-170-17/c
; Sequence 17, Application US/08793170
; Patent No. 5994128
;  GENERAL INFORMATION:
;    APPLICANT:  FALLAUX et al.
;    TITLE OF INVENTION:  PACKAGING SYSTEMS FOR HUMAN RECOMBINANT
;    TITLE OF INVENTION:  ADENOVIRUS TO BE USED IN GENE THERAPY
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
;      STREET:  260 SHERIDAN AVENUE, PO BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,170
;      FILING DATE:  25-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO 97/00326
;      FILING DATE:  14-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201728.3
;      FILING DATE:  26-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95201611.1
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  INGE.002.00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-3377
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-793-170-17

  Query Match            78.9%;  Score 43.4;  DB 2;  Length 50;
  Best Local Similarity  97.8%;  Pred. No. 6.6e-07;
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Job time : 34 secs
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GenCore version 5.1.3

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

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Maximum DB seq length: 2000000000

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Maximum Match 100%
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24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	55	100.0	55	21	AAZ59117	Oligonucleotide HP
	3	55	100.0	55	24	ABK47033	Adenovirus vectro
c	4	51	92.7	55	18	AAT48646	Synthetic haipin o
c	5	51	92.7	55	21	AAZ59116	Oligonucleotide HP
c	6	51	92.7	55	21	AAZ37959	Adenoviral constru
c	7	51	92.7	55	22	AAF30232	Oligonucleotide fo
c	8	51	92.7	55	24	ABK47032	Adenovirus vectro
c	9	43.4	78.9	50	18	AAT48644	Synthetic haipin o
	10	43.4	78.9	50	18	AAT48645	Synthetic haipin o
	11	43.4	78.9	50	21	AAZ37958	Adenoviral constru
c	12	43.4	78.9	50	22	AAF30231	Oligonucleotide fo
c	13	43.4	78.9	50	24	ABK47030	Adenovirus vectro
	14	43.4	78.9	50	24	ABK47031	Adenovirus vectro
	15	43	78.2	54	21	AAZ37960	Adenoviral constru
c	16	42.2	76.7	55	18	AAT48647	Synthetic haipin o
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	18	42.2	76.7	55	21	AAZ59116	Oligonucleotide HP
c	19	42.2	76.7	55	21	AAZ59117	Oligonucleotide HP
	20	42.2	76.7	55	21	AAZ37959	Adenoviral constru
	21	42.2	76.7	55	22	AAF30232	Oligonucleotide fo
	22	42.2	76.7	55	24	ABK47032	Adenovirus vectro
c	23	42.2	76.7	55	24	ABK47033	Adenovirus vectro
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c	25	39.4	71.6	45	21	AAZ37961	DNA molecule conta
c	26	39.4	71.6	45	22	AAF30234	Oligonucleotide fo
c	27	39.4	71.6	45	24	ABK47038	Adenovirus vector
	28	38.6	70.2	50	18	AAT48644	Synthetic haipin o
c	29	38.6	70.2	50	18	AAT48645	Synthetic haipin o
c	30	38.6	70.2	50	21	AAZ37958	Adenoviral constru
	31	38.6	70.2	50	22	AAF30231	Oligonucleotide fo
	32	38.6	70.2	50	24	ABK47030	Adenovirus vectro
c	33	38.6	70.2	50	24	ABK47031	Adenovirus vectro
	34	34.6	62.9	45	21	AAZ59131	Hairpin structure-
	35	34.6	62.9	45	21	AAZ37961	DNA molecule conta
	36	34.6	62.9	45	22	AAF30234	Oligonucleotide fo
	37	34.6	62.9	45	24	ABK47038	Adenovirus vector
c	38	31.4	57.1	49	21	AAZ37957	Adenoviral constru
c	39	30.2	54.9	54	21	AAZ37960	Adenoviral constru
	40	26.6	48.4	49	21	AAZ37957	Adenoviral constru
	41	23.8	43.3	849	24	ABN69129	Streptococcus poly
	42	23.8	43.3	8384	22	AAK82907	Human immune/haema
	43	23.6	42.9	63	24	ABL58790	AAV 5'ITR from vec
	44	23.6	42.9	145	14	AAQ41448	AAV2 inverted term
	45	23.6	42.9	145	16	AAT03385	Strict inverted te

ALIGNMENTS

RESULT 1
AAT48647
ID AAT48647 standard; DNA; 55 BP.
XX
AC AAT48647;
XX
DT 21-MAY-1997 (first entry)
XX
DE Synthetic haipin oligonucleotide HP/cla2.
XX
KW Gene therapy; vaccine; vector; adenovirus; packaging system;
KW hairpin; pICL; ss.
XX
OS Synthetic.
XX
PN WO9700326-A1.
XX
PD 03-JAN-1997.
XX
PF 14-JUN-1996; 96WO-NL00244.
XX
PR 26-JUN-1995; 95EP-0201728.
PR 15-JUN-1995; 95EP-0201611.
XX
PA (INTR-) INTROGENE BV.
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Bout A, Fallaux FJ, Hoeben RC, Valerio D, Van Der EBbAJ;
XX
DR WPI; 1997-077531/07.
XX
PT New packaging cells and nucleic acids for recombinant adenovirus -

PT have no overlapping sequences, prevents homologous recombination;
PT for use in gene therapy and vaccination
XX
PS Disclosure; Page 55; 88pp; English.
XX
CC Synthetic oligonucleotides HP/cla1 (AAT48646) and HP/cla2 (AAT48647)
CC were used to generate a synthetic hairpin. They contain a ClaI
CC recognition site to be used for hairpin formation. The
CC oligonucleotides were annealed and ligated into plasmid pCMV.TK,
CC at the adenovirus inverted terminal repeat, generating
CC pAd-CMV-hcTK. This plasmid was co-transfected with ClaI-digested
CC wild-type adenovirus 4 into 911 cells. A recombinant adenovirus
CC in which the CMV-hcTK expression cassette replaced the E1 sequences
CC was isolated.
XX
SQ Sequence 55 BP; 9 A; 17 C; 17 G; 12 T; 0 other;

Query Match 100.0%; Score 55; DB 18; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55

RESULT 2
AAZ59117
ID AAZ59117 standard; DNA; 55 BP.
XX
AC AAZ59117;
XX
DT 11-APR-2000 (first entry)
XX
DE Oligonucleotide HP/cla2 for generating hairpin structure.
XX
KW Expressible nucleic acid library; gene expression; gene function;
KW capillary formation; cell proliferation; hairpin structure; ss.
XX
OS Synthetic.
XX
PN WO9964582-A2.
XX
PD 16-DEC-1999.
XX
PF 11-JUN-1999; 99WO-NL00367.
XX
PR 12-JUN-1998; 98US-0097239.
XX
PA (INTR-) INTROGENE BV.
XX
PI Schouten G, Vogels R, Bout A, Van Es H;
XX
DR WPI; 2000-097536/08.
XX
PT New library of expressible nucleic acids, useful for high-throughput
PT screening of gene function, especially for identifying therapeutic
PT molecules -
XX
PS Example 3; Page 156; 223pp; English.
XX
CC The invention relates to a library of expressible nucleic acids (NA)
CC which contains many compartments, each comprising at least one vehicle
CC comprising at least one NA, the vehicle being capable of efficiently
CC introducing a NA into a cell for expression. The library is useful for
CC determining the function of one or more nucleic acids within the
CC library, or to screen for an expressible nucleic acid with a particular
CC desired function. It is especially useful for high throughput screening
CC of gene function for functional genomics applications and for screening
CC for nucleic acids with potential therapeutic value. Cell types
CC appropriate for selection of a particular phenotype may be useful for
CC capillary formation and cell proliferation. Oligonucleotides
CC AAZ59116-Z59117 were used to generate a hairpin structure in plasmid
CC pAd-CMV-hcTK. The hairpin structure was used to determine if it could be
CC used to prime reverse strand synthesis on the displaced strand after
CC replication initiation in the adenoviral inverted terminal repeat (ITR).
XX
SQ Sequence 55 BP; 9 A; 17 C; 17 G; 12 T; 0 other;

Query Match 100.0%; Score 55; DB 21; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55

RESULT 3
ABK47033
ID ABK47033 standard; DNA; 55 BP.
XX
AC ABK47033;
XX
DT 05-JUN-2002 (first entry)
XX
DE Adenovirus vectro pICLhac/haw hairpin linker sequence Hp/cla1#2.
XX
KW Adenovirus vector library; ss; linker; high throughput screening;
KW RCA; replication competent adenovirus.
XX
OS Synthetic.
XX
PN US6340595-B1.
XX
PD 22-JAN-2002.
XX
PF 21-JUL-1999; 99US-0358036.
XX
PR 12-JUN-1998; 98US-0097239.
XX
PA (GALA-) GALAPAGOS GENOMICS NV.
XX
PI Vogels R, Bout A, Van Es H, Schouten G;
XX
DR WPI; 2002-224926/28.
XX
PT Library of expressible nucleic acids, useful for determining nucleic
PT acid function, comprises one or more adenoviral vectors capable of
PT transfecting a host cell with the nucleic acid -
XX
PS Example 3; Column 85; 111pp; English.
XX
CC The invention relates to a library (I) of a multitude of unique
CC expressible nucleic acids (NA), comprises a number of compartments
CC (II), each consisting of one or more adenoviral vectors (III)
CC comprising at least one unique NA of (I) in an aqueous medium, where
CC (III) is capable of introducing the NA into a host cell (IV), is
CC capable of expressing the product of the NA in (IV), and is deleted in
CC a portion of the adenoviral genome necessary for replication. Also
CC included is a method for producing the library. The library is useful for
CC determining the function of at least one nucleic acid that is present.
CC The library uses high throughput generation of recombinant adenoviral
CC vector libraries containing one or more sample nucleic acids, followed by
CC high throughput screening of the adenoviral vector libraries in a host to
CC alter the phenotype of the host as a means of assigning a function to
CC expression product(s) of the sample nucleic acids. The entire process
CC lends itself to automation especially when implemented in a 96-well or
CC other multi-well format. The high throughput screening, using a number of
CC different in vitro assays, provides a means of efficiently obtaining
CC functional information in a relatively short period of time. The
CC member(s) of the recombinant adenoviral libraries that exhibit or induce
CC a desired phenotype in a host in vitro or in situ are identified to
CC reduce the libraries to a manageable number of recombinant adenoviral
CC vectors or clones which can be tested in vitro in an animal model.
CC Furthermore, the methods produce RCA-free adenoviral libraries. RCA

```
CC   (replication competent adenovirus) contamination throughout the libraries
CC   could become a major obstacle, especially if libraries are continuously
CC   amplified for use in multiple screening programs. Additionally, a further
CC   advantage is minimisation of the number of steps involved in the process.
CC   There is no requirement for cloning each individual adenovirus before use
CC   in a high throughput screening program. Other systems include one or more
CC   steps in E. coli to achieve homologous recombination for the various
CC   adenoviral plasmids necessary for vector generation. The present
CC   sequence is a linker sequence used in the construction of the adenoviral
CC   vector library of the invention.
XX
SQ   Sequence 55 BP; 9 A; 17 C; 17 G; 12 T; 0 other;

  Query Match             100.0%;  Score 55;  DB 24;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-10;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 4
AAT48646/c
ID   AAT48646 standard; DNA; 55 BP.
XX
AC   AAT48646;
XX
DT   21-MAY-1997  (first entry)
XX
DE   Synthetic haipin oligonucleotide HP/cla1.
XX
KW   Gene therapy; vaccine; vector; adenovirus; packaging system;
KW   hairpin; pICL; ss.
XX
OS   Synthetic.
XX
PN   WO9700326-A1.
XX
PD   03-JAN-1997.
XX
PF   14-JUN-1996;   96WO-NL00244.
XX
PR   26-JUN-1995;   95EP-0201728.
PR   15-JUN-1995;   95EP-0201611.
XX
PA   (INTR-) INTROGENE BV.
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Bout A,  Fallaux FJ,  Hoeben RC,  Valerio D,  Van Der EBbAJ;
XX
DR   WPI; 1997-077531/07.
XX
PT   New packaging cells and nucleic acids for recombinant adenovirus -
PT   have no overlapping sequences, prevents homologous recombination;
PT   for use in gene therapy and vaccination
XX
PS   Disclosure; Page 55; 88pp; English.
XX
CC   Synthetic oligonucleotides HP/cla1 (AAT48646) and HP/cla2 (AAT48647)
CC   were used to generate a synthetic hairpin.  They contain a ClaI
CC   recognition site to be used for hairpin formation.  The
CC   oligonucleotides were annealed and ligated into plasmid pCMV.TK,
CC   at the adenovirus inverted terminal repeat, generating
CC   pAd-CMV-hcTK.  This plasmid was co-transfected with ClaI-digested
CC   wild-type adenovirus 4 into 911 cells.  A recombinant adenovirus
CC   in which the CMV-hcTK expression cassette replaced the E1 sequences
CC   was isolated.
XX
SQ   Sequence 55 BP; 12 A; 17 C; 17 G; 9 T; 0 other;

  Query Match             92.7%;  Score 51;  DB 18;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 5
AAZ59116/c
ID   AAZ59116 standard; DNA; 55 BP.
XX
AC   AAZ59116;
XX
DT   11-APR-2000  (first entry)
XX
DE   Oligonucleotide HP/cla1 for generating hairpin structure.
XX
KW   Expressible nucleic acid library; gene expression; gene function;
KW   capillary formation; cell proliferation; hairpin structure; ss.
XX
OS   Synthetic.
XX
PN   WO9964582-A2.
XX
PD   16-DEC-1999.
XX
PF   11-JUN-1999;   99WO-NL00367.
XX
PR   12-JUN-1998;   98US-0097239.
XX
PA   (INTR-) INTROGENE BV.
XX
PI   Schouten G,  Vogels R,  Bout A,  Van Es H;
XX
DR   WPI; 2000-097536/08.
XX
PT   New library of expressible nucleic acids, useful for high-throughput
PT   screening of gene function, especially for identifying therapeutic
PT   molecules  -
XX
PS   Example 3; Page 156; 223pp; English.
XX
CC   The invention relates to a library of expressible nucleic acids (NA)
CC   which contains many compartments, each comprising at least one vehicle
CC   comprising at least one NA, the vehicle being capable of efficiently
CC   introducing a NA into a cell for expression. The library is useful for
CC   determining the function of one or more nucleic acids within the
CC   library, or to screen for an expressible nucleic acid with a particular
CC   desired function. It is especially useful for high throughput screening
CC   of gene function for functional genomics applications and for  screening
CC   for nucleic acids with potential therapeutic value. Cell types
CC   appropriate for selection of a particular phenotype may be useful for
CC   capillary formation and cell proliferation.  Oligonucleotides
CC   AAZ59116-Z59117 were used to generate a hairpin structure in plasmid
CC   pAd-CMV-hcTK. The hairpin structure was used to determine if it could be
CC   used to prime reverse strand synthesis on the displaced strand after
CC   replication initiation in the adenoviral inverted terminal repeat (ITR).
XX
SQ   Sequence 55 BP; 12 A; 17 C; 17 G; 9 T; 0 other;

  Query Match             92.7%;  Score 51;  DB 21;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 6
AAZ37959/c
ID   AAZ37959 standard; DNA; 55 BP.
XX
```

```
AC   AAZ37959;
XX
DT   07-FEB-2000  (first entry)
XX
DE   Adenoviral construct generating primer Hp/cla1.
XX
KW   Adenoviral vector; replication-defective; adenovirus; ITR; hepatitis;
KW   inverted terminal repeat; encapsulation signal; gene therapy; tumor;
KW   inherited disease; cystic fibrosis; Duchenne molecular dystrophy;
KW   hypercholesterolemia; blood clotting disorder; hemophilia; restenosis;
KW   autoimmune disease; rheumatoid arthritis; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9955132-A2.
XX
PD   04-NOV-1999.
XX
PF   23-APR-1999;   99WO-NL00235.
XX
PR   24-APR-1998;   98US-0065752.
XX
PA   (INTR-) INTROGENE BV.
XX
PI   Vogels R,  Bout A;
XX
DR   WPI; 2000-023229/02.
XX
PT   New recombinant adenovirus vectors, used particularly for gene therapy
PT   for treating inherited or acquired diseases -
XX
PS   Disclosure; Page 118; 161pp; English.
XX
CC   The invention provides methods of producing recombinant adenoviral
CC   vectors (AdV's) for generating replication-defective adenoviruses.
CC   Generating an AdV comprises fusing 2 partially overlapping sequences
CC   nucleic acid molecules that are capable of combining with each other to
CC   allow the generation of a physically linked nucleic acid comprising at
CC   least 2 functional adenoviral inverted terminal repeats (ITRs), a
CC   functional encapsulation signal and a nucleic acid of interest. The
CC   products can be used for gene therapy for treating inherited diseases
CC   e.g. cystic fibrosis, Duchenne molecular dystrophy,
CC   hypercholesterolemia, blood clotting disorders (hemophilia) or acquired
CC   diseases such as tumors, hepatitis, (auto)immune diseases, restenosis, or
CC   rheumatoid arthritis. Sequences AAZ37954-960 represent primers used for
CC   PCR amplification of DNA fragments used for generation of adenoviral
CC   constructs of the invention.
XX
SQ   Sequence 55 BP; 12 A; 17 C; 17 G; 9 T; 0 other;

  Query Match             92.7%;  Score 51;  DB 21;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 7
AAF30232/c
ID   AAF30232 standard; DNA; 55 BP.
XX
AC   AAF30232;
XX
DT   30-APR-2001  (first entry)
XX
DE   Oligonucleotide forming hairpin structure.
XX
KW   Adenovirus; vector; gene therapy; packaging cell; hairpin; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..4
FT                   /*tag=  a
FT                   /note= "single-stranded 5' overhang"
FT   misc_feature    55
FT                   /*tag=  b
FT                   /note= "single-stranded overhang on complementary
FT                          strand of sequence 5'-GTAC-3"
XX
PN   WO200105945-A2.
XX
PD   25-JAN-2001.
XX
PF   19-JUL-2000; 2000WO-EP07074.
XX
PR   19-JUL-1999;   99US-0356575.
XX
PA   (INTR-) INTROGENE BV.
XX
PI   Hoeben RC,  Bout A,  Valerio D,  Van Der Eb AJ,  Schouten G;
PI   Fallaux FJ;
XX
DR   WPI; 2001-147334/15.
XX
PT   Producing recombinant adenovirus for use in gene therapy, comprises
PT   culturing cells containing adenoviral nucleic acid having an
PT   encapsidating signal and inverted terminal repeat, and lacking
PT   overlapping sequences -
XX
PS   Example; Page 39; 97pp; English.
XX
CC   The present sequence is that of an oligonucleotide formed from 2
CC   partially complementary oligonucleotides creating a hairpin
CC   structure.  The oligonucleotide forms an ClaI recognition site
CC   when inserted into the ClaI site of plasmid pICL (see AAF30233).
CC   This was performed as part of an experiment to determine whether
CC   the hairpin could be used as a primer for reverse strand synthesis
CC   on the displaced strand after replication had started from the
CC   inverted terminal repeat (ITR) of the vector.  In adenovirus
CC   infected cells, linear DNA fragments have on one terminus an
CC   adenovirus-derived ITR and at the other terminus a sequence that
CC   can anneal to the same strand, when present in single-stranded
CC   form, thereby generating a hairpin structure, and will be
CC   converted to structures with ITRs at both ends.  The resulting DNA
CC   molecules will replicate by the same mechanism as the wild-type
CC   adenovirus genomes.  The invention provides adenovirus vectors and
CC   packaging cell lines useful in the safe generation of E1-deleted
CC   recombinant adenovirus vectors for gene therapy applications.
CC   Packaging cells contain adenovirus nucleic acids having an
CC   encapsidating signal and ITR, but lack sequences that overlap with
CC   the vector, thereby preventing homologous recombination.
XX
SQ   Sequence 55 BP; 12 A; 17 C; 17 G; 9 T; 0 other;

  Query Match             92.7%;  Score 51;  DB 22;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 8
ABK47032/c
ID   ABK47032 standard; DNA; 55 BP.
XX
AC   ABK47032;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Adenovirus vectro pICLhac/haw hairpin linker sequence Hp/cla1#1.
XX
```

```
KW   Adenovirus vector library; ss; linker; high throughput screening;
KW   RCA; replication competent adenovirus.
XX
OS   Synthetic.
XX
PN   US6340595-B1.
XX
PD   22-JAN-2002.
XX
PF   21-JUL-1999;   99US-0358036.
XX
PR   12-JUN-1998;   98US-0097239.
XX
PA   (GALA-) GALAPAGOS GENOMICS NV.
XX
PI   Vogels R,  Bout A,  Van Es H,  Schouten G;
XX
DR   WPI; 2002-224926/28.
XX
PT   Library of expressible nucleic acids, useful for determining nucleic
PT   acid function, comprises one or more adenoviral vectors capable of
PT   transfecting a host cell with the nucleic acid -
XX
PS   Example 3; Column 85; 111pp; English.
XX
CC   The invention relates to a library (I) of a multitude of unique
CC   expressible nucleic acids (NA), comprises a number of compartments
CC   (II), each consisting of one or more adenoviral vectors (III)
CC   comprising at least one unique NA of (I) in an aqueous medium, where
CC   (III) is capable of introducing the NA into a host cell (IV), is
CC   capable of expressing the product of the NA in (IV), and is deleted in
CC   a portion of the adenoviral genome necessary for replication. Also
CC   included is a method for producing the library. The library is useful for
CC   determining the function of at least one nucleic acid that is present.
CC   The library uses high throughput generation of recombinant adenoviral
CC   vector libraries containing one or more sample nucleic acids, followed by
CC   high throughput screening of the adenoviral vector libraries in a host to
CC   alter the phenotype of the host as a means of assigning a function to
CC   expression product(s) of the sample nucleic acids. The entire process
CC   lends itself to automation especially when implemented in a 96-well or
CC   other multi-well format. The high throughput screening, using a number of
CC   different in vitro assays, provides a means of efficiently obtaining
CC   functional information in a relatively short period of time. The
CC   member(s) of the recombinant adenoviral libraries that exhibit or induce
CC   a desired phenotype in a host in vitro or in situ are identified to
CC   reduce the libraries to a manageable number of recombinant adenoviral
CC   vectors or clones which can be tested in vitro in an animal model.
CC   Furthermore, the methods produce RCA-free adenoviral libraries. RCA
CC   (replication competent adenovirus) contamination throughout the libraries
CC   could become a major obstacle, especially if libraries are continuously
CC   amplified for use in multiple screening programs. Additionally, a further
CC   advantage is minimisation of the number of steps involved in the process.
CC   There is no requirement for cloning each individual adenovirus before use
CC   in a high throughput screening program. Other systems include one or more
CC   steps in E. coli to achieve homologous recombination for the various
CC   adenoviral plasmids necessary for vector generation. The present
CC   sequence is a linker sequence used in the construction of the adenoviral
CC   vector library of the invention.
XX
SQ   Sequence 55 BP; 12 A; 17 C; 17 G; 9 T; 0 other;

  Query Match             92.7%;  Score 51;  DB 24;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 9
AAT48644/c
ID   AAT48644 standard; DNA; 50 BP.
XX
AC   AAT48644;
XX
DT   21-MAY-1997  (first entry)
XX
DE   Synthetic haipin oligonucleotide HP/asp1.
XX
KW   Gene therapy; vaccine; vector; adenovirus; packaging system;
KW   hairpin; pICL; ss.
XX
OS   Synthetic.
XX
PN   WO9700326-A1.
XX
PD   03-JAN-1997.
XX
PF   14-JUN-1996;   96WO-NL00244.
XX
PR   26-JUN-1995;   95EP-0201728.
PR   15-JUN-1995;   95EP-0201611.
XX
PA   (INTR-) INTROGENE BV.
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Bout A,  Fallaux FJ,  Hoeben RC,  Valerio D,  Van Der EBbAJ;
XX
DR   WPI; 1997-077531/07.
XX
PT   New packaging cells and nucleic acids for recombinant adenovirus -
PT   have no overlapping sequences, prevents homologous recombination;
PT   for use in gene therapy and vaccination
XX
PS   Disclosure; Page 55; 88pp; English.
XX
CC   Synthetic oligonucleotides HP/asp1 (AAT48644) and HP/asp2 (AAT48645)
CC   were used to generate a synthetic hairpin, recreating an Asp718
CC   site at one of the termini if inserted in the Asp718 site of
CC   adenovirus minimal vector pICL (see also AAT48630).  Insertion of
CC   the oligonucleotides into pICL generated clone pICLhac (correct
CC   orientation) and pICLhaw (reverse, non-functional orientation).
CC   The constructs were used to demonstrate the competence of a
CC   synthetic DNA sequence, that is capable of forming a hairpin
CC   structure, to serve as a primer for reverse strand synthesis in
CC   the generation of double-stranded DNA molecules in cells that
CC   contain and express adenovirus genes.
XX
SQ   Sequence 50 BP; 10 A; 17 C; 17 G; 6 T; 0 other;

  Query Match             78.9%;  Score 43.4;  DB 18;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 1.8e-06;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           ||||||||||||||||||||||||||||||||||||||||||||| |
Db      49 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 5


RESULT 10
AAT48645
ID   AAT48645 standard; DNA; 50 BP.
XX
AC   AAT48645;
XX
DT   21-MAY-1997  (first entry)
XX
DE   Synthetic haipin oligonucleotide HP/asp2.
XX
KW   Gene therapy; vaccine; vector; adenovirus; packaging system;
KW   hairpin; pICL; ss.
XX
OS   Synthetic.
XX
PN   WO9700326-A1.
```

```
XX
PD   03-JAN-1997.
XX
PF   14-JUN-1996;   96WO-NL00244.
XX
PR   26-JUN-1995;   95EP-0201728.
PR   15-JUN-1995;   95EP-0201611.
XX
PA   (INTR-) INTROGENE BV.
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Bout A, Fallaux FJ, Hoeben RC, Valerio D, Van Der EBbAJ;
XX
DR   WPI; 1997-077531/07.
XX
PT   New packaging cells and nucleic acids for recombinant adenovirus -
PT   have no overlapping sequences, prevents homologous recombination;
PT   for use in gene therapy and vaccination
XX
PS   Disclosure; Page 55; 88pp; English.
XX
CC   Synthetic oligonucleotides HP/asp1 (AAT48644) and HP/asp2 (AAT48645)
CC   were used to generate a synthetic hairpin, recreating an Asp718
CC   site at one of the termini if inserted in the Asp718 site of
CC   adenovirus minimal vector pICL (see also AAT48630). Insertion of
CC   the oligonucleotides into pICL generated clone pICLhac (correct
CC   orientation) and pICLhaw (reverse, non-functional orientation).
CC   The constructs were used to demonstrate the competence of a
CC   synthetic DNA sequence, that is capable of forming a hairpin
CC   structure, to serve as a primer for reverse strand synthesis in
CC   the generation of double-stranded DNA molecules in cells that
CC   contain and express adenovirus genes.
XX
SQ   Sequence 50 BP; 6 A; 17 C; 17 G; 10 T; 0 other;

  Query Match             78.9%;  Score 43.4;  DB 18;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 1.8e-06;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||| |
Db       6 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 50


RESULT 11
AAZ37958
ID   AAZ37958 standard; DNA; 50 BP.
XX
AC   AAZ37958;
XX
DT   07-FEB-2000  (first entry)
XX
DE   Adenoviral construct generating primer Hp/asp2.
XX
KW   Adenoviral vector; replication-defective; adenovirus; ITR; hepatitis;
KW   inverted terminal repeat; encapsulation signal; gene therapy; tumor;
KW   inherited disease; cystic fibrosis; Duchenne molecular dystrophy;
KW   hypercholesterolemia; blood clotting disorder; hemophilia; restenosis;
KW   autoimmune disease; rheumatoid arthritis; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9955132-A2.
XX
PD   04-NOV-1999.
XX
PF   23-APR-1999;   99WO-NL00235.
XX
PR   24-APR-1998;   98US-0065752.
XX
PA   (INTR-) INTROGENE BV.
XX
PI   Vogels R, Bout A;
XX
DR   WPI; 2000-023229/02.
XX
PT   New recombinant adenovirus vectors, used particularly for gene therapy
PT   for treating inherited or acquired diseases -
XX
PS   Disclosure; Page 118; 161pp; English.
XX
CC   The invention provides methods of producing recombinant adenoviral
CC   vectors (AdV's) for generating replication-defective adenoviruses.
CC   Generating an AdV comprises fusing 2 partially overlapping sequences
CC   nucleic acid molecules that are capable of combining with each other to
CC   allow the generation of a physically linked nucleic acid comprising at
CC   least 2 functional adenoviral inverted terminal repeats (ITRs), a
CC   functional encapsulation signal and a nucleic acid of interest. The
CC   products can be used for gene therapy for treating inherited diseases
CC   e.g. cystic fibrosis, Duchenne molecular dystrophy,
CC   hypercholesterolemia, blood clotting disorders (hemophilia) or acquired
CC   diseases such as tumors, hepatitis, (auto)immune diseases, restenosis, or
CC   rheumatoid arthritis. Sequences AAZ37954-960 represent primers used for
CC   PCR amplification of DNA fragments used for generation of adenoviral
CC   constructs of the invention.
XX
SQ   Sequence 50 BP; 6 A; 17 C; 17 G; 10 T; 0 other;

  Query Match             78.9%;  Score 43.4;  DB 21;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 1.8e-06;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||| |
Db       6 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 50


RESULT 12
AAF30231/c
ID   AAF30231 standard; DNA; 50 BP.
XX
AC   AAF30231;
XX
DT   30-APR-2001  (first entry)
XX
DE   Oligonucleotide forming hairpin structure.
XX
KW   Adenovirus; vector; gene therapy; packaging cell; hairpin; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..4
FT                   /*tag= a
FT                   /note= "single-stranded 5' overhang"
FT   misc_feature    50
FT                   /*tag= b
FT                   /note= "single-stranded overhang on complementary
FT                          strand of sequence 5'-GTAC-3"
XX
PN   WO200105945-A2.
XX
PD   25-JAN-2001.
XX
PF   19-JUL-2000; 2000WO-EP07074.
XX
PR   19-JUL-1999;   99US-0356575.
XX
PA   (INTR-) INTROGENE BV.
XX
PI   Hoeben RC, Bout A, Valerio D, Van Der Eb AJ, Schouten G;
PI   Fallaux FJ;
XX
DR   WPI; 2001-147334/15.
XX
PT   Producing recombinant adenovirus for use in gene therapy, comprises
```

PT culturing cells containing adenoviral nucleic acid having an
PT encapsidating signal and inverted terminal repeat, and lacking
PT overlapping sequences -
XX
PS Example; Page 39; 97pp; English.
XX
CC The present sequence is that of an oligonucleotide formed from 2
CC partially complementary oligonucleotides creating a hairpin
CC structure. The oligonucleotide forms an Asp718 recognition site
CC when inserted into the Asp718 site of plasmid pICL (see AAF30233).
CC This was performed as part of an experiment to determine whether
CC the hairpin could be used as a primer for reverse strand synthesis
CC on the displaced strand after replication had started from the
CC inverted terminal repeat (ITR) of the vector. In adenovirus
CC infected cells, linear DNA fragments have on one terminus an
CC adenovirus-derived ITR and at the other terminus a sequence that
CC can anneal to the same strand, when present in single-stranded
CC form, thereby generating a hairpin structure, and will be
CC converted to structures with ITRs at both ends. The resulting DNA
CC molecules will replicate by the same mechanism as the wild-type
CC adenovirus genomes. The invention provides adenovirus vectors and
CC packaging cell lines useful in the safe generation of E1-deleted
CC recombinant adenovirus vectors for gene therapy applications.
CC Packaging cells contain adenovirus nucleic acids having an
CC encapsidating signal and ITR, but lack sequences that overlap with
CC the vector, thereby preventing homologous recombination.
XX
SQ Sequence 50 BP; 10 A; 17 C; 17 G; 6 T; 0 other;

Query Match 78.9%; Score 43.4; DB 22; Length 50;
Best Local Similarity 97.8%; Pred. No. 1.8e-06;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
||||||||||||||||||||||||||||||||||||||||||||| |
Db 49 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 5

RESULT 13
ABK47030/c
ID ABK47030 standard; DNA; 50 BP.
XX
AC ABK47030;
XX
DT 05-JUN-2002 (first entry)
XX
DE Adenovirus vectro pICLhac/haw linker sequence Hp/aspl#1.
XX
KW Adenovirus vector library; ss; linker; high throughput screening;
KW RCA; replication competent adenovirus.
XX
OS Synthetic.
XX
PN US6340595-B1.
XX
PD 22-JAN-2002.
XX
PF 21-JUL-1999; 99US-0358036.
XX
PR 12-JUN-1998; 98US-0097239.
XX
PA (GALA-) GALAPAGOS GENOMICS NV.
XX
PI Vogels R, Bout A, Van Es H, Schouten G;
XX
DR WPI; 2002-224926/28.
XX
PT Library of expressible nucleic acids, useful for determining nucleic
PT acid function, comprises one or more adenoviral vectors capable of
PT transfecting a host cell with the nucleic acid -
XX
PS Example 3; Column 84; 111pp; English.
XX
CC The invention relates to a library (I) of a multitude of unique
CC expressible nucleic acids (NA), comprises a number of compartments
CC (II), each consisting of one or more adenoviral vectors (III)
CC comprising at least one unique NA of (I) in an aqueous medium, where
CC (III) is capable of introducing the NA into a host cell (IV), is
CC capable of expressing the product of the NA in (IV), and is deleted in
CC a portion of the adenoviral genome necessary for replication. Also
CC included is a method for producing the library. The library is useful for
CC determining the function of at least one nucleic acid that is present.
CC The library uses high throughput generation of recombinant adenoviral
CC vector libraries containing one or more sample nucleic acids, followed by
CC high throughput screening of the adenoviral vector libraries in a host to
CC alter the phenotype of the host as a means of assigning a function to
CC expression product(s) of the sample nucleic acids. The entire process
CC lends itself to automation especially when implemented in a 96-well or
CC other multi-well format. The high throughput screening, using a number of
CC different in vitro assays, provides a means of efficiently obtaining
CC functional information in a relatively short period of time. The
CC member(s) of the recombinant adenoviral libraries that exhibit or induce
CC a desired phenotype in a host in vitro or in situ are identified to
CC reduce the libraries to a manageable number of recombinant adenoviral
CC vectors or clones which can be tested in vitro in an animal model.
CC Furthermore, the methods produce RCA-free adenoviral libraries. RCA
CC (replication competent adenovirus) contamination throughout the libraries
CC could become a major obstacle, especially if libraries are continuously
CC amplified for use in multiple screening programs. Additionally, a further
CC advantage is minimisation of the number of steps involved in the process.
CC There is no requirement for cloning each individual adenovirus before use
CC in a high throughput screening program. Other systems include one or more
CC steps in E. coli to achieve homologous recombination for the various
CC adenoviral plasmids necessary for vector generation. The present
CC sequence is a linker sequence used in the construction of the adenoviral
CC vector library of the invention.
XX
SQ Sequence 50 BP; 10 A; 17 C; 17 G; 6 T; 0 other;

Query Match 78.9%; Score 43.4; DB 24; Length 50;
Best Local Similarity 97.8%; Pred. No. 1.8e-06;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
||||||||||||||||||||||||||||||||||||||||||||| |
Db 49 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 5

RESULT 14
ABK47031
ID ABK47031 standard; DNA; 50 BP.
XX
AC ABK47031;
XX
DT 05-JUN-2002 (first entry)
XX
DE Adenovirus vectro pICLhac/haw linker sequence Hp/aspl#2.
XX
KW Adenovirus vector library; ss; linker; high throughput screening;
KW RCA; replication competent adenovirus.
XX
OS Synthetic.
XX
PN US6340595-B1.
XX
PD 22-JAN-2002.
XX
PF 21-JUL-1999; 99US-0358036.
XX
PR 12-JUN-1998; 98US-0097239.
XX
PA (GALA-) GALAPAGOS GENOMICS NV.
XX
PI Vogels R, Bout A, Van Es H, Schouten G;
XX
DR WPI; 2002-224926/28.

```
XX
PT   Library of expressible nucleic acids, useful for determining nucleic
PT   acid function, comprises one or more adenoviral vectors capable of
PT   transfecting a host cell with the nucleic acid -
XX
PS   Example 3; Column 84; 111pp; English.
XX
CC   The invention relates to a library (I) of a multitude of unique
CC   expressible nucleic acids (NA), comprises a number of compartments
CC   (II), each consisting of one or more adenoviral vectors (III)
CC   comprising at least one unique NA of (I) in an aqueous medium, where
CC   (III) is capable of introducing the NA into a host cell (IV), is
CC   capable of expressing the product of the NA in (IV), and is deleted in
CC   a portion of the adenoviral genome necessary for replication. Also
CC   included is a method for producing the library. The library is useful for
CC   determining the function of at least one nucleic acid that is present.
CC   The library uses high throughput generation of recombinant adenoviral
CC   vector libraries containing one or more sample nucleic acids, followed by
CC   high throughput screening of the adenoviral vector libraries in a host to
CC   alter the phenotype of the host as a means of assigning a function to
CC   expression product(s) of the sample nucleic acids. The entire process
CC   lends itself to automation especially when implemented in a 96-well or
CC   other multi-well format. The high throughput screening, using a number of
CC   different in vitro assays, provides a means of efficiently obtaining
CC   functional information in a relatively short period of time. The
CC   member(s) of the recombinant adenoviral libraries that exhibit or induce
CC   a desired phenotype in a host in vitro or in situ are identified to
CC   reduce the libraries to a manageable number of recombinant adenoviral
CC   vectors or clones which can be tested in vitro in an animal model.
CC   Furthermore, the methods produce RCA-free adenoviral libraries. RCA
CC   (replication competent adenovirus) contamination throughout the libraries
CC   could become a major obstacle, especially if libraries are continuously
CC   amplified for use in multiple screening programs. Additionally, a further
CC   advantage is minimisation of the number of steps involved in the process.
CC   There is no requirement for cloning each individual adenovirus before use
CC   in a high throughput screening program. Other systems include one or more
CC   steps in E. coli to achieve homologous recombination for the various
CC   adenoviral plasmids necessary for vector generation. The present
CC   sequence is a linker sequence used in the construction of the adenoviral
CC   vector library of the invention.
XX
SQ   Sequence 50 BP; 6 A; 17 C; 17 G; 10 T; 0 other;

  Query Match             78.9%;  Score 43.4;  DB 24;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 1.8e-06;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||| |
Db       6 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 50


RESULT 15
AAZ37960
ID   AAZ37960 standard; DNA; 54 BP.
XX
AC   AAZ37960;
XX
DT   07-FEB-2000  (first entry)
XX
DE   Adenoviral construct generating primer Hp/cla2.
XX
KW   Adenoviral vector; replication-defective; adenovirus; ITR; hepatitis;
KW   inverted terminal repeat; encapsulation signal; gene therapy; tumor;
KW   inherited disease; cystic fibrosis; Duchenne molecular dystrophy;
KW   hypercholesterolemia; blood clotting disorder; hemophilia; restenosis;
KW   autoimmune disease; rheumatoid arthritis; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9955132-A2.
XX
PD   04-NOV-1999.
XX
PF   23-APR-1999;   99WO-NL00235.
XX
PR   24-APR-1998;   98US-0065752.
XX
PA   (INTR-) INTROGENE BV.
XX
PI   Vogels R,  Bout A;
XX
DR   WPI; 2000-023229/02.
XX
PT   New recombinant adenovirus vectors, used particularly for gene therapy
PT   for treating inherited or acquired diseases -
XX
PS   Disclosure; Page 118; 161pp; English.
XX
CC   The invention provides methods of producing recombinant adenoviral
CC   vectors (AdV's) for generating replication-defective adenoviruses.
CC   Generating an AdV comprises fusing 2 partially overlapping sequences
CC   nucleic acid molecules that are capable of combining with each other to
CC   allow the generation of a physically linked nucleic acid comprising at
CC   least 2 functional adenoviral inverted terminal repeats (ITRs), a
CC   functional encapsulation signal and a nucleic acid of interest. The
CC   products can be used for gene therapy for treating inherited diseases
CC   e.g. cystic fibrosis, Duchenne molecular dystrophy,
CC   hypercholesterolemia, blood clotting disorders (hemophilia) or acquired
CC   diseases such as tumors, hepatitis, (auto)immune diseases, restenosis, or
CC   rheumatoid arthritis. Sequences AAZ37954-960 represent primers used for
CC   PCR amplification of DNA fragments used for generation of adenoviral
CC   constructs of the invention.
XX
SQ   Sequence 54 BP; 9 A; 16 C; 17 G; 12 T; 0 other;

  Query Match             78.2%;  Score 43;  DB 21;  Length 54;
  Best Local Similarity   98.2%;  Pred. No. 2.6e-06;
  Matches   54;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1 GTACATCGATTGACCTAGTGCCGCCCGGG-TTTGCCCGGGCGGCACTAGGTCAAT 54


Search completed: December 27, 2002, 04:46:16
Job time : 171.5 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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(without alignments)
620.636 Million cell updates/sec

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Perfect score: 55
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 363474 seqs, 203117208 residues

Total number of hits satisfying chosen parameters: 726948

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	55	9	US-10-125-751-20	Sequence 20, Appl
2	55	100.0	55	9	US-09-912-552-20	Sequence 20, Appl
3	55	100.0	55	10	US-09-918-029-20	Sequence 20, Appl
4	55	100.0	55	12	US-10-038-271-20	Sequence 20, Appl
c 5	51	92.7	55	9	US-10-125-751-19	Sequence 19, Appl
c 6	51	92.7	55	9	US-09-912-552-19	Sequence 19, Appl
c 7	51	92.7	55	10	US-09-918-029-19	Sequence 19, Appl
c 8	51	92.7	55	10	US-09-900-062-45	Sequence 45, Appl
c 9	51	92.7	55	12	US-10-038-271-19	Sequence 19, Appl
c 10	43.4	78.9	50	9	US-10-125-751-17	Sequence 17, Appl
11	43.4	78.9	50	9	US-10-125-751-18	Sequence 18, Appl
c 12	43.4	78.9	50	9	US-09-912-552-17	Sequence 17, Appl
13	43.4	78.9	50	9	US-09-912-552-18	Sequence 18, Appl
c 14	43.4	78.9	50	10	US-09-918-029-17	Sequence 17, Appl
15	43.4	78.9	50	10	US-09-918-029-18	Sequence 18, Appl
16	43.4	78.9	50	10	US-09-900-062-44	Sequence 44, Appl
c 17	43.4	78.9	50	12	US-10-038-271-17	Sequence 17, Appl
18	43.4	78.9	50	12	US-10-038-271-18	Sequence 18, Appl
19	43	78.2	54	10	US-09-900-062-46	Sequence 46, Appl
20	42.2	76.7	55	9	US-10-125-751-19	Sequence 19, Appl
c 21	42.2	76.7	55	9	US-10-125-751-20	Sequence 20, Appl
22	42.2	76.7	55	9	US-09-912-552-19	Sequence 19, Appl
c 23	42.2	76.7	55	9	US-09-912-552-20	Sequence 20, Appl
24	42.2	76.7	55	10	US-09-918-029-19	Sequence 19, Appl
c 25	42.2	76.7	55	10	US-09-918-029-20	Sequence 20, Appl
26	42.2	76.7	55	10	US-09-900-062-45	Sequence 45, Appl
27	42.2	76.7	55	12	US-10-038-271-19	Sequence 19, Appl
c 28	42.2	76.7	55	12	US-10-038-271-20	Sequence 20, Appl
c 29	39.4	71.6	45	9	US-10-125-751-22	Sequence 22, Appl
c 30	39.4	71.6	45	10	US-09-918-029-22	Sequence 22, Appl
c 31	39.4	71.6	45	10	US-09-900-062-47	Sequence 47, Appl
c 32	39.4	71.6	45	12	US-10-038-271-22	Sequence 22, Appl
33	38.6	70.2	50	9	US-10-125-751-17	Sequence 17, Appl
c 34	38.6	70.2	50	9	US-10-125-751-18	Sequence 18, Appl
35	38.6	70.2	50	9	US-09-912-552-17	Sequence 17, Appl
c 36	38.6	70.2	50	9	US-09-912-552-18	Sequence 18, Appl
37	38.6	70.2	50	10	US-09-918-029-17	Sequence 17, Appl
c 38	38.6	70.2	50	10	US-09-918-029-18	Sequence 18, Appl
c 39	38.6	70.2	50	10	US-09-900-062-44	Sequence 44, Appl
40	38.6	70.2	50	12	US-10-038-271-17	Sequence 17, Appl
c 41	38.6	70.2	50	12	US-10-038-271-18	Sequence 18, Appl
c 42	36.2	65.8	45	9	US-09-912-552-22	Sequence 22, Appl
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44	34.6	62.9	45	10	US-09-918-029-22	Sequence 22, Appl
45	34.6	62.9	45	10	US-09-900-062-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-125-751-20
; Sequence 20, Application US/10125751
; Patent No. US20020173039A1
; GENERAL INFORMATION:
; APPLICANT: Fallaux, Frits J.
; APPLICANT: Hoeben, Robert C.
; APPLICANT: Bout, Abraham
; APPLICANT: Valerio, Domenico
; APPLICANT: Van der Eb, Alex J.
; TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO
; TITLE OF INVENTION: BE USED
; TITLE OF INVENTION: IN GENE THERAPY
; FILE REFERENCE: 3833.2US
; CURRENT APPLICATION NUMBER: US/10/125,751
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 09/506,548
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: PCT/NL96/00244
; PRIOR FILING DATE: 1996-06-14
; PRIOR APPLICATION NUMBER: EP 95201728.3
; PRIOR FILING DATE: 1995-06-26
; PRIOR APPLICATION NUMBER: EP 95201611.1
; PRIOR FILING DATE: 1995-06-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 20
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Description of Artificial Sequence: primer HP/cla2
US-10-125-751-20

Query Match 100.0%; Score 55; DB 9; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 2
US-09-912-552-20
; Sequence 20, Application US/09912552
; Publication No. US20020187553A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits
;  APPLICANT:  Hoeben, Robert
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  van der Eb, Alex
;  APPLICANT:  Schouten, Govert
;  TITLE OF INVENTION: PACKAGING SYSTEMS
;  FILE REFERENCE: 2578-3935US
;  CURRENT APPLICATION NUMBER: US/09/912,552
;  CURRENT FILING DATE:  2001-07-02
;  PRIOR APPLICATION NUMBER: US/09/356,575
;  PRIOR FILING DATE: 1999-07-19
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Derived from Adenovirus
US-09-912-552-20

  Query Match             100.0%;  Score 55;  DB 9;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-12;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 3
US-09-918-029-20
; Sequence 20, Application US/09918029
; Patent No. US20020102732A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO
;  TITLE OF INVENTION:  BE USED
;  TITLE OF INVENTION:  IN GENE THERAPY
;  FILE REFERENCE: 3833.2US
;  CURRENT APPLICATION NUMBER: US/09/918,029
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: 09/506,548
;  PRIOR FILING DATE: 2000-02-16
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 20
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: primer HP/cla2
US-09-918-029-20

  Query Match             100.0%;  Score 55;  DB 10;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-12;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 4
US-10-038-271-20
; Sequence 20, Application US/10038271
; Patent No. US20020151032A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO BE USED
;  TITLE OF INVENTION:  GENE THERAPY
;  FILE REFERENCE: 3833.1US
;  CURRENT APPLICATION NUMBER: US/10/038,271
;  CURRENT FILING DATE:  2001-10-23
;  PRIOR APPLICATION NUMBER: 09/333,820
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: US 08/793,170
;  PRIOR FILING DATE: 1997-03-25
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 20
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: primer HP/cla2
US-10-038-271-20

  Query Match             100.0%;  Score 55;  DB 12;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-12;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55


RESULT 5
US-10-125-751-19/c
; Sequence 19, Application US/10125751
; Patent No. US20020173039A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
```

```
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO
;  TITLE OF INVENTION:  BE USED
;  TITLE OF INVENTION:  IN GENE THERAPY
;  FILE REFERENCE: 3833.2US
;  CURRENT APPLICATION NUMBER: US/10/125,751
;  CURRENT FILING DATE:  2002-04-18
;  PRIOR APPLICATION NUMBER: 09/506,548
;  PRIOR FILING DATE: 2000-02-16
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 19
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: PCT primer HP/cla1
US-10-125-751-19

  Query Match             92.7%;  Score 51;  DB 9;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 5e-11;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 6
US-09-912-552-19/c
; Sequence 19, Application US/09912552
; Publication No. US20020187553A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits
;  APPLICANT:  Hoeben, Robert
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  van der Eb, Alex
;  APPLICANT:  Schouten, Govert
;  TITLE OF INVENTION: PACKAGING SYSTEMS
;  FILE REFERENCE: 2578-3935US
;  CURRENT APPLICATION NUMBER: US/09/912,552
;  CURRENT FILING DATE:  2001-07-02
;  PRIOR APPLICATION NUMBER: US/09/356,575
;  PRIOR FILING DATE: 1999-07-19
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Derived from Adenovirus
US-09-912-552-19

  Query Match             92.7%;  Score 51;  DB 9;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 5e-11;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 7
US-09-918-029-19/c
; Sequence 19, Application US/09918029
; Patent No. US20020102732A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO
;  TITLE OF INVENTION:  BE USED
;  TITLE OF INVENTION:  IN GENE THERAPY
;  FILE REFERENCE: 3833.2US
;  CURRENT APPLICATION NUMBER: US/09/918,029
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: 09/506,548
;  PRIOR FILING DATE: 2000-02-16
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 19
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: PCT primer HP/cla1
US-09-918-029-19

  Query Match             92.7%;  Score 51;  DB 10;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 5e-11;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 8
US-09-900-062-45/c
; Sequence 45, Application US/09900062
; Patent No. US20020119942A1
; GENERAL INFORMATION:
;  APPLICANT: Vogels, Ronald
;  APPLICANT:  Bout, Abraham
;  TITLE OF INVENTION: Packaging systems for human recombinant adenovirus to
;  TITLE OF INVENTION:  be used in gene therapy
;  FILE REFERENCE: P20879US02
;  CURRENT APPLICATION NUMBER: US/09/900,062
;  CURRENT FILING DATE:  2001-07-06
;  PRIOR APPLICATION NUMBER: US/09/065,752
;  PRIOR FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: (1)..(55)
;   OTHER INFORMATION: /No. US20020119942Ale="primer HP/cla1"
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;  OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-900-062-45

  Query Match             92.7%;  Score 51;  DB 10;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 5e-11;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 9
US-10-038-271-19/c
; Sequence 19, Application US/10038271
; Patent No. US20020151032A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO BE USED IN
;  TITLE OF INVENTION:  GENE THERAPY
;  FILE REFERENCE: 3833.1US
;  CURRENT APPLICATION NUMBER: US/10/038,271
;  CURRENT FILING DATE:  2001-10-23
;  PRIOR APPLICATION NUMBER: 09/333,820
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: US 08/793,170
;  PRIOR FILING DATE: 1997-03-25
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 19
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: PCT primer HP/cla1
US-10-038-271-19

  Query Match             92.7%;  Score 51;  DB 12;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 5e-11;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 ATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 5


RESULT 10
US-10-125-751-17/c
; Sequence 17, Application US/10125751
; Patent No. US20020173039A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO
;  TITLE OF INVENTION:  BE USED
;  TITLE OF INVENTION:  IN GENE THERAPY
;  FILE REFERENCE: 3833.2US
;  CURRENT APPLICATION NUMBER: US/10/125,751
;  CURRENT FILING DATE:  2002-04-18
;  PRIOR APPLICATION NUMBER: 09/506,548
;  PRIOR FILING DATE: 2000-02-16
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 17
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: PCT primer HP/asp1
US-10-125-751-17

  Query Match             78.9%;  Score 43.4;  DB 9;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 4e-08;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||| |
Db      49 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 5


RESULT 11
US-10-125-751-18
; Sequence 18, Application US/10125751
; Patent No. US20020173039A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO
;  TITLE OF INVENTION:  BE USED
;  TITLE OF INVENTION:  IN GENE THERAPY
;  FILE REFERENCE: 3833.2US
;  CURRENT APPLICATION NUMBER: US/10/125,751
;  CURRENT FILING DATE:  2002-04-18
;  PRIOR APPLICATION NUMBER: 09/506,548
;  PRIOR FILING DATE: 2000-02-16
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 18
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence:  PCT primer HP/asp2
US-10-125-751-18

  Query Match             78.9%;  Score 43.4;  DB 9;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 4e-08;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||| |
Db       6 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 50
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RESULT 12
US-09-912-552-17/c
; Sequence 17, Application US/09912552
; Publication No. US20020187553A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits
;  APPLICANT:  Hoeben, Robert
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  van der Eb, Alex
;  APPLICANT:  Schouten, Govert
;  TITLE OF INVENTION: PACKAGING SYSTEMS
;  FILE REFERENCE: 2578-3935US
;  CURRENT APPLICATION NUMBER: US/09/912,552
;  CURRENT FILING DATE:  2001-07-02
;  PRIOR APPLICATION NUMBER: US/09/356,575
;  PRIOR FILING DATE: 1999-07-19
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Derived from Adenovirus
US-09-912-552-17

  Query Match             78.9%;  Score 43.4;  DB 9;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 4e-08;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||| |
Db      49 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 5


RESULT 13
US-09-912-552-18
; Sequence 18, Application US/09912552
; Publication No. US20020187553A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits
;  APPLICANT:  Hoeben, Robert
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  van der Eb, Alex
;  APPLICANT:  Schouten, Govert
;  TITLE OF INVENTION: PACKAGING SYSTEMS
;  FILE REFERENCE: 2578-3935US
;  CURRENT APPLICATION NUMBER: US/09/912,552
;  CURRENT FILING DATE:  2001-07-02
;  PRIOR APPLICATION NUMBER: US/09/356,575
;  PRIOR FILING DATE: 1999-07-19
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Derived from Adenovirus
US-09-912-552-18

  Query Match             78.9%;  Score 43.4;  DB 9;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 4e-08;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||| |
Db       6 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 50


RESULT 14
US-09-918-029-17/c
; Sequence 17, Application US/09918029
; Patent No. US20020102732A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO
;  TITLE OF INVENTION:  BE USED
;  TITLE OF INVENTION:  IN GENE THERAPY
;  FILE REFERENCE: 3833.2US
;  CURRENT APPLICATION NUMBER: US/09/918,029
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: 09/506,548
;  PRIOR FILING DATE: 2000-02-16
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 17
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence: PCT primer HP/aspl
US-09-918-029-17

  Query Match             78.9%;  Score 43.4;  DB 10;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 4e-08;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           |||||||||||||||||||||||||||||||||||||||||||| |
Db      49 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 5


RESULT 15
US-09-918-029-18
; Sequence 18, Application US/09918029
; Patent No. US20020102732A1
; GENERAL INFORMATION:
;  APPLICANT: Fallaux, Frits J.
;  APPLICANT:  Hoeben, Robert C.
;  APPLICANT:  Bout, Abraham
;  APPLICANT:  Valerio, Domenico
;  APPLICANT:  Van der Eb, Alex J.
;  TITLE OF INVENTION: PACKAGING SYSTEMS FOR HUMAN RECOMBINANT ADENOVIRUS TO
;  TITLE OF INVENTION:  BE USED
;  TITLE OF INVENTION:  IN GENE THERAPY
;  FILE REFERENCE: 3833.2US
;  CURRENT APPLICATION NUMBER: US/09/918,029
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;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: 09/506,548
;  PRIOR FILING DATE: 2000-02-16
;  PRIOR APPLICATION NUMBER: PCT/NL96/00244
;  PRIOR FILING DATE: 1996-06-14
;  PRIOR APPLICATION NUMBER: EP 95201728.3
;  PRIOR FILING DATE: 1995-06-26
;  PRIOR APPLICATION NUMBER: EP 95201611.1
;  PRIOR FILING DATE: 1995-06-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 18
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Description of Artificial Sequence:  PCT primer HP/asp2
US-09-918-029-18

  Query Match             78.9%;  Score 43.4;  DB 10;  Length 50;
  Best Local Similarity   97.8%;  Pred. No. 4e-08;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
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Db       6 TGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAGT 50


Search completed: December 27, 2002, 06:18:34
Job time : 36 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 04:38:01 ; Search time 1321.5 Seconds
(without alignments)
674.046 Million cell updates/sec

Title: US-09-918-029-20
Perfect score: 55
Sequence: 1 gtacatcgattgacctagtg.....ccgggcggcactaggtcaat 55

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24.8	45.1	756	10	BE254363	BE254363 601109113
	2	24.2	44.0	590	17	AZ205863	AZ205863 SP_0105_A
c	3	24.2	44.0	794	10	BE294341	BE294341 601172854
	4	23.8	43.3	174	17	AQ588337	AQ588337 CITBI-E1-
	5	23.8	43.3	885	9	AL564683	AL564683 AL564683
c	6	23.8	43.3	885	9	AL564683	AL564683 AL564683
c	7	23.8	43.3	1108	14	BQ887187	BQ887187 AGENCOURT
	8	23.6	42.9	319	17	AQ357767	AQ357767 CITBI-E1-
	9	23.6	42.9	372	13	BI716319	BI716319 1031009F0
c	10	23.2	42.2	409	13	BG955901	BG955901 CM3-CT060
	11	23.2	42.2	977	14	BQ672537	BQ672537 AGENCOURT
	12	23	41.8	317	14	R77680	R77680 yi62c09.s1
c	13	23	41.8	596	12	BG194272	BG194272 RST13417
	14	23	41.8	822	17	CNS021IX	AL176946 Tetraodon
	15	23	41.8	906	17	CNS03A5J	AL234784 Tetraodon
c	16	23	41.8	1488	12	BG845293	BG845293 1024009F0
	17	22.8	41.5	344	9	AA081549	AA081549 zn21g07.r
c	18	22.8	41.5	453	17	TA313C10Q	AL490228 T. brucei
	19	22.8	41.5	526	14	BQ812739	BQ812739 1030032A0
	20	22.8	41.5	565	12	BE725257	BE725257 894082A06
c	21	22.8	41.5	592	9	AL703582	AL703582 DKFZp686C
	22	22.8	41.5	658	12	BG724427	BG724427 602693726
	23	22.8	41.5	749	12	BG722376	BG722376 602693574
	24	22.8	41.5	749	12	BG844791	BG844791 1024007G1
	25	22.8	41.5	755	12	BG719715	BG719715 602690436
c	26	22.8	41.5	810	12	BG671517	BG671517 DRNBTE09
	27	22.8	41.5	814	12	BG717933	BG717933 602693988
	28	22.8	41.5	816	13	BI464399	BI464399 603204058
	29	22.8	41.5	820	13	BG923596	BG923596 602823455
c	30	22.8	41.5	959	14	BQ679905	BQ679905 AGENCOURT
c	31	22.6	41.1	534	17	AQ838837	AQ838837 HS_4716_A
	32	22.6	41.1	556	13	BM105647	BM105647 509147 MA
	33	22.6	41.1	582	9	AI981396	AI981396 pat.pk005
c	34	22.6	41.1	749	12	BG844791	BG844791 1024007G1
c	35	22.6	41.1	798	12	BF696525	BF696525 602125006
	36	22.6	41.1	1051	9	AL549845	AL549845 AL549845
	37	22.6	41.1	1115	13	BM546853	BM546853 AGENCOURT
c	38	22.6	41.1	1374	14	BM906040	BM906040 AGENCOURT
	39	22.4	40.7	447	12	BG792158	BG792158 UTSW_H2E8
c	40	22.4	40.7	452	17	AQ878057	AQ878057 HS_2160_A
c	41	22.4	40.7	560	12	BF930291	BF930291 RC5-NT018
	42	22.4	40.7	652	12	BF204631	BF204631 601867053
	43	22.4	40.7	741	12	BG828205	BG828205 602753589
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ALIGNMENTS

RESULT 1
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LOCUS BE254363 756 bp mRNA linear EST 13-JUL-2000
DEFINITION 601109113F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350090 5', mRNA sequence.
ACCESSION BE254363
VERSION BE254363.1 GI:9124791
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM145 row: i column: 03
High quality sequence stop: 668.
FEATURES Location/Qualifiers
source 1. .756
/organism="Homo sapiens"

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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3350090"
                     /clone_lib="NIH_MGC_16"
                     /tissue_type="retinoblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      115 a    197 c    275 g    169 t
ORIGIN

  Query Match             45.1%;  Score 24.8;  DB 10;  Length 756;
  Best Local Similarity   72.7%;  Pred. No. 2.8e+02;
  Matches   32;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy       8 GATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGT 51
            || || ||| |||| ||  ||||  ||||||| ||| || |||
Db     185 GACTGGCCTGGTGCAGCTGGGGCGGTGCCCGGCGGGCCCTGGGT 228


RESULT 2
AZ205863
LOCUS       AZ205863                590 bp    DNA     linear   GSS 31-AUG-2000
DEFINITION  SP_0105_A1_F05_T7A Strongylocentrotus purpuratus, purple sea urchin
            , sperm genomic BAC library Strongylocentrotus purpuratus genomic
            clone Plate=105 Col=9 Row=K, DNA sequence.
ACCESSION   AZ205863
VERSION     AZ205863.1  GI:8415870
KEYWORDS    GSS.
SOURCE      Strongylocentrotus purpuratus.
  ORGANISM  Strongylocentrotus purpuratus
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoida;
            Strongylocentrotidae; Strongylocentrotus.
REFERENCE   1  (bases 1 to 590)
  AUTHORS   Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
            Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray
            ,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. and
            Hood,L.
  TITLE     A sea urchin genome project: Sequence scan, virtual map, and
            additional resources
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
  MEDLINE   20402566
COMMENT     Contact: Cameron, RA, Davidson, EH, Hood, L
            Division of Biology 156-29
            California Institute of Technology
            Pasadena California 91125, USA
            Tel: (626) 395-8421
            Fax: (626) 793-3047
            Email: acameron@caltech.edu
            Plate: 105  row: K  column: 9
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 590.
FEATURES             Location/Qualifiers
     source          1. .590
                     /organism="Strongylocentrotus purpuratus"
                     /db_xref="taxon:7668"
                     /clone="Plate=105 Col=9 Row=K"
                     /clone_lib="Strongylocentrotus purpuratus, purple sea
                     urchin, sperm genomic BAC library"
                     /note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                     DH10B"
BASE COUNT      163 a    157 c    110 g    159 t      1 others
ORIGIN

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  Best Local Similarity   66.0%;  Pred. No. 4.2e+02;
  Matches   35;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy       3 ACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
             ||||| | | ||  ||||| | | | ||  ||| || |  ||||||  | |||
Db     165 ACATCAACTCACACAGTGCTGACAGAGCGATGCACGTGTCGCACTAACTGAAT 217


RESULT 3
BE294341/c
LOCUS       BE294341                794 bp    mRNA    linear   EST 20-JUL-2000
DEFINITION  601172854F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528349 5',
            mRNA sequence.
ACCESSION   BE294341
VERSION     BE294341.1  GI:9177788
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 794)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM197  row: 1  column: 14
            High quality sequence stop: 605.
FEATURES             Location/Qualifiers
     source          1. .794
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3528349"
                     /clone_lib="NIH_MGC_17"
                     /tissue_type="rhabdomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      193 a    226 c    216 g    159 t
ORIGIN

  Query Match             44.0%;  Score 24.2;  DB 10;  Length 794;
  Best Local Similarity   71.1%;  Pred. No. 4.5e+02;
  Matches   32;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       6 TCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGG 50
             ||  | | |||||||||| | |||| | | |||||| | || | ||
Db     684 TCCCTGGGCCTAGTGCCCCTCGGGATGTTCCCGGGGGCCATTGGG 640


RESULT 4
AQ588337
LOCUS       AQ588337                174 bp    DNA     linear   GSS 07-JUN-1999
DEFINITION  CITBI-E1-2644P17.TR CITBI-E1 Homo sapiens genomic clone 2644P17,
            DNA sequence.
ACCESSION   AQ588337
VERSION     AQ588337.1  GI:5015017
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

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REFERENCE   1  (bases 1 to 174)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2644P17.TF
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .174
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                     /db_xref="taxon:9606"
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                     /cell_type="sperm"
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ORIGIN

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  Best Local Similarity   72.1%;  Pred. No. 4.5e+02;
  Matches   31;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      10 TTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTC 52
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Db      76 TTGCCTTAGTACCTACCTGGCTTTCCCCGGAGAGCAGAAGGTC 118


RESULT 5
AL564683
LOCUS       AL564683                885 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL564683 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM007YK12 3
            prime, mRNA sequence.
ACCESSION   AL564683
VERSION     AL564683.1  GI:12915335
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 885)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .885
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DM007YK12"
                     /clone_lib="LTI_NFL001_NBC4"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT       166 a    253 c    263 g    159 t     44 others
ORIGIN

  Query Match             43.3%;  Score 23.8;  DB 9;  Length 885;
  Best Local Similarity   66.0%;  Pred. No. 6.2e+02;
  Matches   31;  Conservative    2;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       8 GATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAA 54
           | |||| | |||||||| | |||  || || ||| |||: | :| |
Db     561 GCTTGAACAAGTGCCGCAGGTGCTGAGCTCGCGCGACACKSGCKCCA 607


RESULT 6
AL564683/c
LOCUS       AL564683                885 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL564683 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM007YK12 3
            prime, mRNA sequence.
ACCESSION   AL564683
VERSION     AL564683.1  GI:12915335
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 885)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DM007YK12"
                     /clone_lib="LTI_NFL001_NBC4"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT       166 a    253 c    263 g    159 t     44 others
ORIGIN

  Query Match             43.3%;  Score 23.8;  DB 9;  Length 885;
  Best Local Similarity   66.0%;  Pred. No. 6.2e+02;
  Matches   31;  Conservative    2;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       8 GATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAA 54
           | | |: | :||| ||| || |||  || |  |||||||| | ||||
Db     609 GGTGGMGCSMGTGTCGCGCGAGCTCAGCACCTGCGGCACTTGTTCAA 563


RESULT 7
BQ887187/c
LOCUS       BQ887187                1108 bp    mRNA    linear   EST 16-AUG-2002
```

```
DEFINITION  AGENCOURT_8678059 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6380936
            5', mRNA sequence.
ACCESSION   BQ887187
VERSION     BQ887187.1  GI:22279201
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1108)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2570  row: f  column: 09
            High quality sequence start: 112
            High quality sequence stop: 276.
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     source          1. .1108
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6380936"
                     /clone_lib="NIH_MGC_40"
                     /tissue_type="carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California,  Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life  Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      197 a    363 c    388 g    160 t
ORIGIN

  Query Match            43.3%;  Score 23.8;  DB 14;  Length 1108;
  Best Local Similarity  66.7%;  Pred. No. 6.5e+02;
  Matches   34;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy       4 CATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAA 54
           ||||||    || |  ||| |||||| |||| ||   |||| | ||  |||
Db     711 CATCGACCCCCCCAAGGCCACCCGGGGTTTGGCCCCTCGGCGCAAGTCCAA 661


RESULT 8
AQ357767
LOCUS       AQ357767                319 bp    DNA     linear   GSS 24-JAN-1999
DEFINITION  CITBI-E1-2535A15.TR CITBI-E1 Homo sapiens genomic clone 2535A15,
            DNA sequence.
ACCESSION   AQ357767
VERSION     AQ357767.1  GI:4184940
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 319)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2535A15.TF
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .319
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="2535A15"
                     /clone_lib="CITBI-E1"
                     /sex="male"
                     /cell_type="sperm"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
BASE COUNT       64 a     86 c     93 g     76 t
ORIGIN

  Query Match            42.9%;  Score 23.6;  DB 17;  Length 319;
  Best Local Similarity  64.8%;  Pred. No. 5.9e+02;
  Matches   35;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy       1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAA 54
           | | || ||| || ||  |||| | | ||  || || ||| || | || || ||
Db      92 GGAAATGGATAGATCTCCTGCCTCACAGGAATTCCCAGGGTGGGAGTATGTAAA 145


RESULT 9
BI716319
LOCUS       BI716319                372 bp    mRNA    linear   EST 19-SEP-2001
DEFINITION  1031009F01.xl C. reinhardtii CC-1690, Stress II (normalized),
            Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION   BI716319
VERSION     BI716319.1  GI:15692014
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii.
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre
            ,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants. Project: 1031
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Charles Hauser
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000
            Tel: 919 613 8159
            Fax: 919 613 8177
            Email: chauser@duke.edu.
FEATURES             Location/Qualifiers
     source          1. .372
                     /organism="Chlamydomonas reinhardtii"
                     /strain="CC-1690 wild type mt+ 21gr"
                     /db_xref="taxon:3055"
                     /clone_lib="C. reinhardtii CC-1690, Stress II (normalized
                     ), Lambda Zap II"
                     /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                     XhoI; Stress condition II library, constructed by John
                     Davies and Jeffrey McDermott, combines cDNAs from CC-1690
                     cells grown to mid-log phase in TAP (NH4+ - containing)
                     and shifted to TAP - NO3- (24hrs); H2 production
                     conditions (0, 12hr, 24hr) see Melis et al.,(2000) Plant
                     Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
```

sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

BASE COUNT 76 a 116 c 97 g 83 t
ORIGIN

Query Match 42.9%; Score 23.6; DB 13; Length 372;
Best Local Similarity 64.8%; Pred. No. 6.1e+02;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```
Qy       2 TACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAAT 55
           || ||| | |    || |||| || |||||||| |||||  | |  || | ||
Db     234 TAAATCTACTCGGGTAATGCCCCCTGGGCTTTGTTCGGGCACCTCCCGGGCGAT 287
```

RESULT 10
BG955901/c
LOCUS BG955901 409 bp mRNA linear EST 12-JUN-2001
DEFINITION CM3-CT0607-130201-747-f01 CT0607 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG955901
VERSION BG955901.1 GI:14374072
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 409)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-CT0607-130201-747-f01&t3=2001-02-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 176.

FEATURES Location/Qualifiers
source 1. .409
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0607"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 86 a 113 c 136 g 74 t
ORIGIN

Query Match 42.2%; Score 23.2; DB 13; Length 409;
Best Local Similarity 70.5%; Pred. No. 8.4e+02;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```
Qy       4 CATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACT 47
           || || || ||| || |||   ||| |||  ||| |||| ||||
Db     256 CAGCGTTTCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCACT 213
```

RESULT 11
BQ672537
LOCUS BQ672537 977 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT_8488986 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6256457 5', mRNA sequence.
ACCESSION BQ672537
VERSION BQ672537.1 GI:21783371
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 977)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM2409 row: c column: 18
High quality sequence stop: 405.

FEATURES Location/Qualifiers
source 1. .977
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6256457"
/clone_lib="NIH_MGC_102"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 194 a 332 c 279 g 171 t 1 others
ORIGIN

Query Match 42.2%; Score 23.2; DB 14; Length 977;
Best Local Similarity 70.5%; Pred. No. 1e+03;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```
Qy       2 TACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCA 45
           | |  || |   || |||||||||||||  |||||| | | ||
Db     810 TTCCGCGCTCCCCCAAGTGCCGCCCGGGCGGTGCCCGCGGGACA 853
```

RESULT 12
R77680
LOCUS R77680 317 bp mRNA linear EST 07-JUN-1995
DEFINITION yi62c09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143824 3' similar to gb:U11863 AMILORIDE-SENSITIVE AMINE OXIDASE (HUMAN);, mRNA sequence.
ACCESSION R77680
VERSION R77680.1 GI:852790

```
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 317)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 858
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 858   Std Error: 0.00
            Seq primer: Promega -21m13
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .317
                     /organism="Homo sapiens"
                     /db_xref="GDB:553028"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:143824"
                     /clone_lib="Soares placenta Nb2HP"
                     /sex="Female"
                     /dev_stage="placenta obtained at birth (full term)"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo.  "
BASE COUNT       54 a     68 c    110 g     56 t     29 others
ORIGIN

  Query Match             41.8%;  Score 23;  DB 14;  Length 317;
  Best Local Similarity   64.0%;  Pred. No. 9.3e+02;
  Matches   32;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy       1 GTACATCGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGG 50
           ||  || |  || || ||||  |||| ||   | || ||| || ||| ||
Db      12 GTTTATTGNCTGCCCCAGTGAGGCCCCGGGGNTNCCGGGGAGGAACTGGG 61


RESULT 13
BG194272/c
LOCUS       BG194272                596 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST13417 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG194272
VERSION     BG194272.1  GI:13715959
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 596)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 596.
FEATURES             Location/Qualifiers
     source          1. .596
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      181 a    140 c    126 g    148 t      1 others
ORIGIN

  Query Match             41.8%;  Score 23;  DB 12;  Length 596;
  Best Local Similarity   68.1%;  Pred. No. 1.1e+03;
  Matches   32;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       8 GATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCAA 54
           | ||| | ||||| | |||  ||| ||||  |||   ||  ||||||
Db      54 GTTTGGCTTAGTGGCTCCCTTGCTCTGCCAAGGCTAGACCTGGTCAA 8


RESULT 14
CNS021IX
LOCUS       CNS021IX                822 bp    DNA     linear   GSS 12-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            225L17 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL176946
VERSION     AL176946.1  GI:7815003
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 822)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 822)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 822)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
```

```
           genome. For more information, please take a look at
           http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .822
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="225L17"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG225CF09SP1-end :
                     PUC-Ori"
BASE COUNT       65 a    292 c    269 g    185 t     11 others
ORIGIN

  Query Match             41.8%;  Score 23;  DB 17;  Length 822;
  Best Local Similarity   68.1%;  Pred. No. 1.1e+03;
  Matches   32;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       7 CGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCA 53
           || | | ||| |  |||| ||| ||| ||||| |||||  | |  ||
Db     312 CGCTCGGCCTTGGCCCGCTCGGCCTTGGCCCGCGCGGCCTTGGCCCA 358


RESULT 15
CNS03A5J
LOCUS       CNS03A5J                 906 bp    DNA     linear   GSS 15-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            008N24 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL234784
VERSION     AL234784.1  GI:7893919
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 906)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 906)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .906
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="008N24"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG008DG12SP1-end :
                     PUC-Ori"
BASE COUNT       92 a    313 c    284 g    214 t      3 others
ORIGIN

  Query Match             41.8%;  Score 23;  DB 17;  Length 906;
  Best Local Similarity   68.1%;  Pred. No. 1.1e+03;
  Matches   32;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       7 CGATTGACCTAGTGCCGCCCGGGCTTTGCCCGGGCGGCACTAGGTCA 53
           || | | ||| |  |||| ||| ||| ||||| |||||  | |  ||
Db     396 CGCTCGGCCTTGGCCCGCTCGGCCTTGGCCCGCGCGGCCTTGGCCCA 442


Search completed: December 27, 2002, 06:15:36
Job time : 1324.5 secs
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